

SCORE Search Results Details for Application 10687035 and Search Result 20070607\_154734\_us-10-687-035-1\_copy\_14\_452.rag.

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This page gives you Search Results detail for the Application 10687035 and Search Result 20070607\_154734\_us-10-687-035-1\_copy\_14\_452.rag.

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OM protein - protein search, using sw model

Run on: June 7, 2007, 17:43:31 ; Search time 212 Seconds (without alignments)  
1013.289 Million cell updates/sec

Title: US-10-687-035-1\_COPY14\_452  
Perfect score: 2321  
Sequence: 1 FTHRSSVSTTSTPGTPVYL.....HGVTQGFVLDRLDSLFING 439

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_200701: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*  
9: geneseqp2005s: \*  
10: geneseqp2006s: \*  
11: geneseqp2007s: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2321	100.0	748	8	ADS94302	AdS94302 CA 125/O7
2	2321	100.0	772	3	AA12553	Ab12553 Human ova
3	2321	100.0	772	5	ABP30897	Abp30897 0772p clo
4	2321	100.0	772	7	ADA08541	Ada08541 Human ova
5	2321	100.0	772	7	ADF08884	Adf08884 Secreted
6	2321	100.0	772	7	ADG46171	Adg46171 Human ova
7	2321	100.0	772	9	ADX17767	Adx17767 Human ova
8	2321	100.0	809	8	ADS94303	AdS94303 CA 125/O7
9	2321	100.0	833	3	AA12554	Ab12554 Human ova
10	2321	100.0	833	5	ABP30898	Abp30898 0772p clo
11	2321	100.0	833	7	ADA08542	Ada08542 Human ova
12	2321	100.0	833	7	ADF08885	Adf08885 Secreted
13	2321	100.0	833	7	ADG46172	Adg46172 Human ova
14	2321	100.0	833	9	ADX17768	Adx17768 Human ova
15	2321	100.0	914	3	AA12552	Ab12552 Human ova
16	2321	100.0	914	4	AB99203	Ab99203 Human ova
17	2321	100.0	914	5	ABP30968	Abp30968 Hypotheti
18	2321	100.0	914	5	ABP30896	Abp30896 0772p pro
19	2321	100.0	914	5	ADU01425	Adu01425 Breast ca
20	2321	100.0	914	5	AD241689	Ad241689 Human bre
21	2321	100.0	914	7	ADA08631	Ada08631 Human O77
22	2321	100.0	914	7	ADA08465	Ada08465 Human ova
23	2321	100.0	914	7	ADF08974	Adf08974 Secreted
24	2321	100.0	914	7	ADF08808	Adf08808 Secreted
25	2321	100.0	914	7	ADG46095	Adg46095 Human ova
26	2321	100.0	914	8	ADN40451	Adn40451 Human bre
27	2321	100.0	914	9	ADX17691	Adx17691 Human ova
28	2321	100.0	914	9	ADX17857	Adx17857 Partial h
29	2321	100.0	1485	8	ADP81174	Adp81174 Protein o
30	2317	99.8	748	10	AEK19871	Aek19871 CA 125 po
31	2317	99.8	1889	6	AAE34700	Aae34700 Protein e
32	2317	99.8	1890	5	ABG96381	Abg96381 Human ova
33	2317	99.8	1890	8	ADM12352	Adm12352 Human CA1
34	2317	99.8	1890	8	ADQ38574	Ado38574 Ovarian c
35	2317	99.8	1890	10	AEF01059	Aef01059 Ovarian c
36	2317	99.8	6995	9	AEC60057	Aec60057 Human muc
37	2317	99.8	6995	10	AEI74820	Aei74820 Cancer-as
38	2312	99.6	3451	5	ABP31026	Abp31026 Amino aci
39	2312	99.6	3451	7	ADA08748	Ada08748 Human O77
40	2312	99.6	3451	7	ADF09091	Adf09091 Secreted
41	2312	99.6	3451	9	ADX17974	Adx17974 Human ova
42	2301	99.1	1148	4	AB958636	Ab958636 Human pro
43	2301	99.1	1148	4	ABB50283	Abb50283 HOST-1 ov
44	2301	99.1	1148	5	ABG96380	Abg96380 Human ova
45	2301	99.1	1148	5	ABP30964	Abp30964 Truncated

ALIGNMENTS

RESULT 1  
ADS94302  
ID ADS94302 standard; protein; 748 AA.

XX AD594302;  
AC  
XX  
DT  
XX 02-DEC-2004 (first entry)  
XX  
DE CA 125/O772P 3-repeat amino acid sequence SEQ ID NO:1.  
XX  
XX antibody; antigen-binding antibody fragment;  
KW cell-associated CA 125/O772P; monoclonal antibody; cytostatic;  
KW immunostimulant; mediator of lysis; tumour; cell proliferative disorder;  
KW cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;  
KW ovarian cancer.  
XX  
XX Synthetic.  
OS  
XX WO2004035537-A2.  
PN  
XX 29-APR-2004.  
XX  
XX 15-OCT-2003; 2003WO-US032945.  
XX  
XX 16-OCT-2002; 2002US-0418828P.  
PR  
XX 10-JUL-2003; 2003US-0485986P.  
XX  
XX (EURO-) EUROCELTIQUE SA.  
PA  
XX Albane EF, Soltis DA;  
PI  
XX WPI: 2004-357171/33.  
DR  
XX  
XX Novel isolated antibody, or antigen-binding antibody fragment binding  
PT with cell-associated CA 125/O772P polypeptide relative to shed CA  
PT 125/O772 polypeptide, useful for ameliorating cervical or ovarian cancer.  
XX  
XX Example; SEQ ID NO 1: 153pp; English.  
PS  
XX  
XX The present invention describes an isolated antibody, or an antigen-  
CC binding antibody fragment (I), that preferentially binds cell-associated  
CC CA 125/O772P polypeptide relative to shed CA 125/O772 polypeptide. Also  
CC described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)  
CC a monoclonal antibody that competes with binding of (II); (3) a hybridoma  
CC as deposited in (II); (4) an isolated nucleic acid molecule (III)  
CC comprising a nucleotide sequence that encodes a variable chain region of  
CC (I); (5) a pharmaceutical composition comprising an antibody or an  
CC antigen-binding antibody fragment that preferentially binds cell-  
CC associated CA 125/O772P polypeptide relative to shed CA 125/O772P  
CC polypeptide, and a carrier; (6) a pharmaceutical composition comprising a  
CC monoclonal antibody or an antigen-binding monoclonal antibody fragment  
CC that preferentially binds cell-associated CA 125/O772P polypeptide  
CC relative to shed CA 125/O772P polypeptide, and a carrier; (7) an article  
CC of manufacture (IV) comprising packaging material and a composition  
CC comprising an antibody, or an antigen-binding antibody fragment that  
CC preferentially binds cell-associated CA 125/O772P relative to shed CA  
CC 125/O772P, and a carrier contained within the packaging material, and  
CC composition in a form suitable for administration to a subject; (8) a  
CC fusion polypeptide (V) comprising an antibody, or an antigen-binding  
CC antibody fragment, which preferentially binds cell-associated CA  
CC 125/O772P relative to shed CA 125/O772P operably linked to a heterologous  
CC agent; (9) ameliorating (M1) a symptom of a CA 125/O772P-related disorder  
CC ; (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1,  
CC 725.1, 869, 7F10, 8A1, 8AC3, 15C9, 8E3, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9,

CC 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding  
CC antibody fragment; (II) an antibody or antigen binding antibody fragment  
CC that competes with (VI); and (12) a pharmaceutical composition comprising  
CC (VI) and a carrier. (I) has cytostatic activity, and can be used as an  
CC immunostimulant and a mediator of lysis of positive tumour cell. (I) is  
CC useful for ameliorating a symptom of a CA 125/O77P-related disorder which  
CC is a cell proliferative disorder such as cancer, cervical or uterine  
CC cancer, breast or lung cancer or ovarian cancer. (V) is useful  
CC diagnostically for monitoring the development or progression of cancer or  
CC tumour as part of clinical testing procedure. The present sequence  
CC represents the CA 125/O772P 3-repeat amino acid sequence, which is used  
CC in the exemplification of the present invention.  
XX  
SQ Sequence 748 AA;  
Query Match 100.0%; Score 2321; DB 8; Length 748;  
Best Local Similarity 100.0%; Pred. No. 3.4e-212;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTHRSSVSTTSGPTTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRVEENWPG 60  
DB 14 FTHRSSVSTTSGPTTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRVEENWPG 73  
QY 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPPTGP 120  
DB 74 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPPTGP 133  
QY 121 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
DB 134 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193  
QY 181 INLRVYMDWQPGSGLKENITDNVMKLLSPLEFRSSLGARYTCRVIALRSVKNGAETR 240  
DB 194 INLRVYMDWQPGSGLKENITDNVMKLLSPLEFRSSLGARYTCRVIALRSVKNGAETR 253  
QY 241 VDLICTYLOPLSGCLPIKOVFHELSQOHTGHTRLGPLYSLDKDSLYLNGYNEPGDEPPT 300  
DB 254 VDLICTYLOPLSGCLPIKOVFHELSQOHTGHTRLGPLYSLDKDSLYLNGYNEPGDEPPT 313  
QY 301 TPKPATTFPLPULSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360  
DB 314 TPKPATTFPLPULSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 373  
QY 361 PLFKSSMGPFYLGQQLISLRPEKDGATGVDTCTYHPDPVPGGLDIOQLYWELSQLTH 420  
DB 374 PLFKSSMGPFYLGQQLISLRPEKDGATGVDTCTYHPDPVPGGLDIOQLYWELSQLTH 433  
QY 421 GVTOLGFYVLDKDSLIFNG 439  
DB 434 GVTOLGFYVLDKDSLIFNG 452  
RESULT 2  
AAB12553  
ID AAB12553 standard; protein; 772 AA.  
XX  
AC AAB12553;  
DT  
XX 07-NOV-2000 (first entry)  
XX  
DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:388.

XX	Human: ovarian carcinoma; ovarian cancer; therapy; diagnosis; tumour antigen; identification; cytostatic; gene therapy; vaccine.
KW	Homo sapiens.
OS	WO2000036107-A2.
XX	22-JUN-2000.
PN	17-DEC-1999; 99WO-US030270.
PD	17-DEC-1998; 98US-00215681.
PF	17-DEC-1999; 98US-00216003.
PR	23-JUN-1999; 99US-00338933.
PR	24-SEP-1999; 99US-00404879.
XX	(CORI-) CORIXA CORP.
PA	Mitcham JL, King GE, Algate PA, Frudakis TN;
PI	WPI: 2000-431589/37.
XX	N-PSDB; AAA70074.
DR	Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of cancer, preferably ovarian cancer.
XX	Example 2; Page 197-200; 299pp; English.
PS	The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (for its variants).
XX	Ovarian carcinoma proteins, and polynucleotides encoding them, have cytotstatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention
CC	exemplification of the present invention
XX	Sequence 772 AA;
SQ	Query Match 100.0%; Score 2321; DB 3; Length 772; Best Local Similarity 100.0%; Pred. No. 3.5e-212; Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGFSAAASHLLILFTLFTINLRYEENWMPG 60 
Db	159 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGFSAAASHLLILFTLFTINLRYEENWMPG 218 
Oy	61 SRKFTNTERVQGLLRPLEKNTSGVPLYSGCCRLTLRPEKDGEGVDAICTHRPDPDTPG 120 
Db	219 SRKFTNTERVQGLLRPLEKNTSGVPLYSGCCRLTLRPEKDGEGVDAICTHRPDPDTPG 278 
Oy	121 GLDREQLYLELSOLTHSIHELGPYTLDRDSLYNGFTHRSSVPTTSTGVVSEEPFLNFT 180 
Db	279 GLDREQLYLELSOLTHSIHELGPYTLDRDSLYNGFTHRSSVPTTSTGVVSEEPFLNFT 338 
Oy	181 INNLRYMADWGQPSGLKFNITDNWKHLLSPILFQRSSLGARYTGCGRVIALRSVKNGAETR 240 
Db	339 INNLRYMADWGQPSGLKFNITDNWKHLLSPILFQRSSLGARYTGCGRVIALRSVKNGAETR 398 

CC proteins, T cell populations and antigen presenting cells that express  
CC the polypeptides are useful for stimulating an immune response in a  
CC patient and treating ovarian cancer. This sequence represents protein  
CC related to the invention  
XX  
XX  
SQ Sequence 772 AA;  
  
Query Match 100.0%; Score 2321; DB 5; Length 772;  
Best Local Similarity 100.0%; Pred. No. 3.5e-212;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60  
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218  
  
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 120  
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 278  
  
Qy 121 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
Db 279 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338  
  
Qy 181 INNLRYMADMGQPSLKFNITDNVMKHLSPFLQFSSILGARYTGCRRVIALRSVKNGAETR 240  
Db 339 INNLRYMADMGQPSLKFNITDNVMKHLSPFLQFSSILGARYTGCRRVIALRSVKNGAETR 398  
  
Qy 241 VDLCTYLOPLSGPLPIKOVFHELSQOOTHGTRIGPYSLDKDSLXLNGYNEPGDEPPT 300  
Db 399 VDLCTYLOPLSGPLPIKOVFHELSQOOTHGTRIGPYSLDKDSLXLNGYNEPGDEPPT 458  
  
Qy 301 TKPATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLRL 360  
Db 459 TKPATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLRL 518  
  
Qy 361 PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYMWLSQTH 420  
Db 519 PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYMWLSQTH 578  
  
Qy 421 GVTQLGYVLDRLSLFNG 439  
Db 579 GVTQLGYVLDRLSLFNG 597  
  
RESULT 4  
ID ADA08541  
XX ADA08541 standard; protein; 772 AA.  
AC ADA08541;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human ovarian carcinoma antigen O772P #1.  
XX  
KW human; gene therapy; ovarian cancer; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US2003091580-A1.  
XX  
PD 15-MAY-2003.

XX  
PF 17-JUL-2001; 2001US-00907969.  
XX  
PR 18-JUN-2001; 2001US-00884441.  
XX  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
XX  
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;  
PI Reed SG, Vedwick TS, Carter D, Hill P, Albone E;  
XX  
XX WPI; 2003-532352/50.  
XX  
XX New isolated O772P polypeptides and polynucleotides, useful in gene  
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian  
PT cancer.  
XX  
PS Example 2; SEQ ID NO 388; 371pp; English.  
XX  
CC The invention relates to an isolated O772P polypeptide, which has the  
CC structure fully defined in the specification. The composition containing  
CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells  
CC or antigen presenting cells are useful for stimulating an immune response  
CC and treating ovarian cancer. Detecting the presence of the  
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian  
CC carcinoma cDNAs and protein cDNAs were identified using microarray  
CC technology. The present sequence represents a human ovarian carcinoma  
CC antigen.  
XX  
SQ Sequence 772 AA;  
  
Query Match 100.0%; Score 2321; DB 7; Length 772;  
Best Local Similarity 100.0%; Pred. No. 3.5e-212;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60  
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218  
  
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 120  
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 278  
  
Qy 121 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
Db 279 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338  
  
Qy 181 INNLRYMADMGQPSLKFNITDNVMKHLSPFLQFSSILGARYTGCRRVIALRSVKNGAETR 240  
Db 339 INNLRYMADMGQPSLKFNITDNVMKHLSPFLQFSSILGARYTGCRRVIALRSVKNGAETR 398  
  
Qy 241 VDLCTYLOPLSGPLPIKOVFHELSQOOTHGTRIGPYSLDKDSLXLNGYNEPGDEPPT 300

Db 399 VDLCTYQLPSGPGIPKQVHELSQOQTHGTRGLGYSLDKDSLYLNGYNPEGDEPPT 458  
QY 301 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 360  
Db 459 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518  
QY 361 PLFKSSMGPFYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 420  
Db 519 PLFKSSMGPFYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 578  
QY 421 GVTQLGYVLDRLDSLIFNG 439  
Db 579 GVTQLGYVLDRLDSLIFNG 597

RESULT 5  
ADF08884  
ID ADF08884 standard; protein; 772 AA.  
XX  
AC ADF08884;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Secreted ovarian carcinoma antigen seqid 388.  
XX  
KW gene therapy; protein therapy; vaccine; antibody inhibition;  
KW breast cancer; restorative therapy; diagnostic agent; immunoassay;  
KW secreted ovarian carcinoma antigen.  
XX  
OS Homo sapiens.  
XX  
PN US2003124140-A1.  
XX  
PD 03-JUL-2003.  
XX  
PF 17-JUL-2002; 2002US-00198053.  
XX  
PR 17-DEC-1998; 98US-00215681.  
PR 17-DEC-1998; 98US-00216003.  
PR 23-JUN-1999; 99US-00338933.  
PR 24-SEP-1999; 99US-00404879.  
PR 17-JUL-2000; 2000US-00617747.  
PR 10-AUG-2000; 2000US-00636801.  
PR 20-SEP-2000; 2000US-00667857.  
PR 04-APR-2001; 2001US-00827271.  
PR 18-JUN-2001; 2001US-00884441.  
PR 17-JUL-2001; 2001US-00907969.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Bangur CS, Retter KW, Fanger GR, Hill P;  
XX  
DR WPI: 2003-897152/82.  
DR N-PSDB; ADF08881.  
XX  
PT Oncogenic nucleic acids useful for the prevention, diagnosis and  
PT treatment of breast cancer.  
XX  
PS Example 2; SEQ ID NO 388; 399pp; English.  
XX

CC The invention describes nucleic acids (I) and the polypeptides (II) they  
CC encode. The nucleic acids (I) may be used for preventing, diagnosing and  
CC treating diseases related to their aberrant expression i.e. breast  
CC cancers. For example, (I) and (II) may be used to treat disorders  
CC associated with decreased expression by rectifying mutations or deletions  
CC in a patient's genome that affect the activity of (II) by expressing  
CC inactive proteins or to supplement the patients own production of (III).  
CC Additionally, (I) may be used to produce (II), by inserting (I) into a  
CC host cell and culturing the cell to express the protein (II). (I) And its  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays to detect and quantitate the presence of similar nucleic acids in  
CC samples, and therefore which patients may be in need of restorative  
CC therapy. The host cell may also be used as antigens in the production of  
CC antibodies against (II) and in assays to identify modulators of (II)'s  
CC expression and activity. The anti-(II) antibodies, agonists and  
CC antagonists may be used to regulate expression and activity and as  
CC diagnostic agents for detecting the presence of (II) in samples (e.g. by  
CC immunoassay). This sequence represents a secreted ovarian carcinoma  
CC antigen.  
XX  
XX Sequence 772 AA;  
QY Query Match 100.0%; Score 2321; DB 7; Length 772;  
Best Local Similarity 100.0%; Fred. No. 3.5e-212; Mismatches 0; Indels 0; Gaps 0;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSASHLLILFTLNFTLNRYEENWPG 60  
Db 159 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSASHLLILFTLNFTLNRYEENWPG 218  
QY 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLRPEKDGATGVDAICTHRPDPTGP 120  
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLRPEKDGATGVDAICTHRPDPTGP 278  
QY 121 GLDREQLYLELSQLTHSITELGPLYTLDRDSLXVNGFTHRSSVPTTSTGVSEEPFTLNFT 180  
Db 279 GLDREQLYLELSQLTHSITELGPLYTLDRDSLXVNGFTHRSSVPTTSTGVSEEPFTLNFT 338  
QY 181 INNLRYMADMGQPGSLKFNITDNVMKLLSPLFQRSSILGARYTCRVIALRSVKNGAETR 240  
Db 339 INNLRYMADMGQPGSLKFNITDNVMKLLSPLFQRSSILGARYTCRVIALRSVKNGAETR 398  
QY 241 VDLCTYQLPSGPGIPKQVHELSQOQTHGTRGLGYSLDKDSLYLNGYNPEGDEPPT 300  
Db 399 VDLCTYQLPSGPGIPKQVHELSQOQTHGTRGLGYSLDKDSLYLNGYNPEGDEPPT 458  
QY 301 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 360  
Db 459 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518  
QY 361 PLFKSSMGPFYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 420  
Db 519 PLFKSSMGPFYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 578  
QY 421 GVTQLGYVLDRLDSLIFNG 439  
Db 579 GVTQLGYVLDRLDSLIFNG 597

RESULT 6  
ADG46171

ID	ADG46171 standard; protein; 772 AA.
XX	
AC	ADG46171;
XX	
DT	26-FEB-2004 (first entry)
XX	
DE	Human ovarian carcinoma polypeptide #2.
XX	
KW	Human; ovarian carcinoma; O8E; ovarian cancer; secreted tumour antigen;
KW	cytostatic; 0772P.
XX	
OS	Homo sapiens.
XX	
PN	US2003165504-A1.
XX	
PD	04-SEP-2003.
XX	
PF	04-APR-2001; 2001US-00827271.
XX	
PR	17-DEC-1998; 98US-00215681.
PR	17-DEC-1998; 98US-00216003.
PR	23-JUN-1999; 99US-00338933.
PR	24-SEP-1999; 99US-00404879.
PR	17-JUL-2000; 2000US-00617747.
PR	10-AUG-2000; 2000US-00636801.
PR	20-SEP-2000; 2000US-00667857.
XX	
PA	(RETT/) RETTER M W.
PA	(FANG/) FANGER G R.
XX	
PI	Retter MW, Fanger GR;
XX	
DR	WPI; 2003-898035/82.
XX	
PT	New isolated O8E or 0772P polypeptides, useful for diagnosing,
PT	preventing, treating and monitoring cancer, e.g. ovarian cancer,
XX	stimulating the immune response in patient.
XX	
PS	Claim 5; SEQ ID NO 388; 290pp; English.
XX	
CC	The invention relates to human ovarian carcinoma polypeptides, designated
CC	O8E or 0772P, and the polynucleotides encoding them. The invention also
CC	relates to methods for inhibiting the development of cancer, e.g. ovarian
CC	cancer in a patient, methods for stimulating and/or expanding T cells and
CC	methods for identifying secreted tumour antigens. The polypeptides,
CC	compositions, antibodies to the polypeptides and methods are useful for
CC	diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
CC	cancer. The composition is particularly useful for stimulating an immune
CC	response in patient. This sequence represents a human ovarian carcinoma
CC	polypeptide of the invention.
XX	
SQ	Sequence 772 AA:
	Query Match 100.0%; Score 2321; DB 7; Length 772;
	Best Local Similarity 100.0%; Pred. No. 3.Se-212;
	Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFLNFTITNLRYEENWMPG 60
DB	159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFLNFTITNLRYEENWMPG 218

QY	61 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLTLRLPEKDEATGVDAICTHRPDPPTGP 120
DB	219 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLTLRLPEKDEATGVDAICTHRPDPPTGP 278
QY	121 GLDREQLYELSQLTHSITELGPYTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
DB	279 GLDREQLYELSQLTHSITELGPYTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
QY	181 INNLRYMADMGQPGSLKENITDNWKHLSPLFQRSSILGARYTGCRVIALRSVKNGAETR 240
DB	339 INNLRYMADMGQPGSLKENITDNWKHLSPLFQRSSILGARYTGCRVIALRSVKNGAETR 398
QY	241 VDLLCTYLQPLSGPGLPIKQVFHELSSQOOTHGITRLGPIYSLDKDSLYLNGYNERPDPDEPT 300
DB	399 VDLLCTYLQPLSGPGLPIKQVFHELSSQOOTHGITRLGPIYSLDKDSLYLNGYNERPDPDEPT 458
QY	301 TPKPATTFELPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATENSTEGVIGHLLR 360
DB	459 TPKPATTFELPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATENSTEGVIGHLLR 518
QY	361 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 420
DB	519 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 578
QY	421 GVTQLGFVYLDROSLFING 439
DB	579 GVTQLGFVYLDROSLFING 597
RESULT 7	
ADX17767	
ID	ADX17767 standard; protein; 772 AA.
XX	
AC	ADX17767;
XX	
DT	21-APR-2005 (first entry)
XX	
DE	Human ovarian carcinoma antigen cDNA 0772P clone 21013 encoded protein.
XX	
KW	diagnosis; cytostatic; immunostimulant; gene therapy; tumor;
KW	ovarian tumor; cancer; carcinoma; antigen.
XX	
OS	Homo sapiens.
XX	
PN	US2005031634-A1.
XX	
PD	10-FEB-2005.
XX	
PF	02-JUN-2004; 2004US-00860790.
XX	
PR	17-DEC-1998; 98US-00216003.
PR	23-JUN-1999; 99US-00338933.
PR	24-SEP-1999; 99US-00404879.
PR	17-JUL-2000; 2000US-00617747.
PR	10-AUG-2000; 2000US-00636801.
PR	20-SEP-2000; 2000US-00667857.
PR	04-APR-2001; 2001US-00827271.
PR	18-JUN-2001; 2001US-00884441.
PR	17-JUL-2001; 2001US-00907969.
PR	17-JUL-2002; 2002US-00198053.
XX	



CC agent; (9) ameliorating (M1) a symptom of a CA 125/O772P-related disorder  
CC ; (10) a monoclonal antibody (VI) chosen from 325.1.1, 621.1, 633.1, 654.1,  
CC 725.1.1, 8G9, 7F10, 8A1, 8AC3, 15C9, 8E3, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9,  
CC 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding  
CC antibody fragment; (11) an antibody or antigen binding antibody fragment  
CC that competes with (VI); and (12) a pharmaceutical composition comprising  
CC (VI) and a carrier. (I) has cytostatic activity, and can be used as an  
CC immunostimulant and a mediator of lysis of positive tumour cell. (I) is  
CC useful for ameliorating a symptom of a CA 125/O77P-related disorder which  
CC is a cell proliferative disorder such as cancer, cervical or uterine  
CC cancer, breast or lung cancer or ovarian cancer. (VI) is useful  
CC diagnostically for monitoring the development or progression of cancer or  
CC tumour as part of clinical testing procedure. The present sequence  
CC represents the CA 125/O772P 3-repeat TM amino acid sequence, which is  
CC used in the exemplification of the present invention.  
XX  
SQ Sequence 809 AA;

Query Match 100.0%; Score 2321; DB 8; Length 809;  
Best Local Similarity 100.0%; Pred. No. 3.8e-212;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTPTGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60  
DB 14 FTHRSSVSTTPTGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 73  
QY 61 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120  
DB 74 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 133  
QY 121 GLDREQLYLELSQTHSITELGPTYLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
DB 134 GLDREQLYLELSQTHSITELGPTYLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193  
QY 181 INNLRYMADMGPGLSKFNITDNVMKHLSPFLFORSSIGARYTGCRVIALRSYKNGAETR 240  
DB 194 INNLRYMADMGPGLSKFNITDNVMKHLSPFLFORSSIGARYTGCRVIALRSYKNGAETR 253  
QY 241 VDLICTYIQPLSGPLPIKQVFHELSSQOOTHGITRLGYSIDKDSLYLNGYNEFGPDEPPT 300  
DB 254 VDLICTYIQPLSGPLPIKQVFHELSSQOOTHGITRLGYSIDKDSLYLNGYNEFGPDEPPT 313  
QY 301 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360  
DB 314 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 373  
QY 361 PLFOKSSMGPFYLGCCQLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDITQOLYWELSQLTH 420  
DB 374 PLFOKSSMGPFYLGCCQLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDITQOLYWELSQLTH 433  
QY 421 GVTQLGYVYLDROSLFNG 439  
DB 434 GVTQLGYVYLDROSLFNG 452

RESULT 9  
ID AAB12554  
XX AAB12554 standard; protein: 833 AA.  
AC AAB12554;  
XX

DT 07-NOV-2000 (first entry)  
XX Human ovarian carcinoma antigen O772P protein SEQ ID NO:389.  
DE  
XX Human: ovarian carcinoma; ovarian cancer; therapy: diagnosis;  
KW tumour antigen; identification; cytostatic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX WO200036107-A2.  
XX  
PD 22-JUN-2000.  
XX  
PF 17-DEC-1999; 99WO-US030270.  
XX  
PR 17-DEC-1998; 98US-00215681.  
PR 17-DEC-1998; 98US-00216003.  
PR 23-JUN-1999; 99US-00338933.  
PR 24-SEP-1999; 99US-00404879.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Mitcham JL, King GE, Algate PA, Frudakis TN;  
XX  
XX WPI; 2000-431589/37.  
DR N-PSDB; AAA70075.  
XX  
XX Immunogenic portion of an ovarian carcinoma protein and the nucleic acid  
PT encoding it, useful for the diagnosis, prevention and treatment of  
PT cancer, preferably ovarian cancer.  
XX  
PS Example 2; Page 200-203; 299pp; English.  
XX  
CC The present invention describes an isolated polypeptide comprising an  
CC immunogenic portion of an ovarian carcinoma protein (or its variants).  
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have  
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian  
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful  
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian  
CC cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human  
CC ovarian carcinoma polynucleotides and proteins used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 833 AA;

Query Match 100.0%; Score 2321; DB 3; Length 833;  
Best Local Similarity 100.0%; Pred. No. 4e-212;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTHRSSVSTTPTGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60  
DB 78 FTHRSSVSTTPTGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137  
QY 61 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120  
DB 138 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 197  
QY 121 GLDREQLYLELSQTHSITELGPTYLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
DB 198 GLDREQLYLELSQTHSITELGPTYLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257



Qy	181	INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR	240
Db	258	INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR	317
Qy	241	VDLLCTYLQPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT	300
Db	318	VDLLCTYLQPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT	377
Qy	301	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSPOMGKGSATNSTEGVLQHLR	360
Db	378	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSPOMGKGSATNSTEGVLQHLR	437
Qy	361	PLFQKSSMGPFYLGCOLISLRPEKDGAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH	420
Db	438	PLFQKSSMGPFYLGCOLISLRPEKDGAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH	497
Qy	421	GVTQLGEYVLDKDSLFING	439
Db	498	GVTQLGEYVLDKDSLFING	516
RESULT 10			
ABP30898	ABP30898 standard; protein: 833 AA.		
AC	ABP30898;		
DT	02-JUL-2002 (first entry)		
XX	0772P clone 21003.		
KW	Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.		
OS	Homo sapiens.		
PN	W0200206317-A2.		
PD	24-JAN-2002.		
PF	17-JUL-2001; 2001WO-US022635.		
PR	17-JUL-2000; 2000US-00617747.		
PR	10-AUG-2000; 2000US-00636801.		
PR	20-SEP-2000; 2000US-00667857.		
PR	04-APR-2001; 2001US-00827271.		
PR	18-JUN-2001; 2001US-00884441.		
PA	(CORI-) CORIXA CORP.		
PI	Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;		
PI	Reed SG, Vedvick TS, Carter D, Hill P, Albone E;		
XX	WPI; 2002-164781/21.		
DR	N-PSDB; ABN72969.		
XX	Polypeptides comprising an immunogenic portion of an ovarian carcinoma protein or its variants, useful for stimulating an immune response in a patient and treating ovarian cancer.		
PS	Example 2; Page 316-318; 408pp; English.		
XX			

CC	This invention relates to polypeptides comprising an immunogenic portion of an ovarian carcinoma protein which acts as an immunostimulant and is cytostatic. The polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells that express the polypeptides are useful for stimulating an immune response in a patient and treating ovarian cancer. This sequence represents protein CC related to the invention		
XX			
Qy	Sequence 833 AA;		
Query Match	100.08;	Score 2321;	DB 5; Length 833;
Best Local Similarity	100.08;	Pred. No. 4e-212;	
Matches 439;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG	60
Db	78	FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG	137
Qy	61	SRKFNITERVLOGLLRPLFKNTSVGPLYSGCRLTLRPEKDGEATGDAICTHRPDPFG	120
Db	138	SRKFNITERVLOGLLRPLFKNTSVGPLYSGCRLTLRPEKDGEATGDAICTHRPDPFG	197
Qy	121	GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT	180
Db	198	GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT	257
Qy	181	INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR	240
Db	258	INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR	317
Qy	241	VDLLCTYLQPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT	300
Db	318	VDLLCTYLQPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT	377
Qy	301	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSPOMGKGSATNSTEGVLQHLR	360
Db	378	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSPOMGKGSATNSTEGVLQHLR	437
Qy	361	PLFQKSSMGPFYLGCOLISLRPEKDGAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH	420
Db	438	PLFQKSSMGPFYLGCOLISLRPEKDGAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH	497
Qy	421	GVTQLGEYVLDKDSLFING	439
Db	498	GVTQLGEYVLDKDSLFING	516
RESULT 11			
ADA08542	ADA08542 standard; protein: 833 AA.		
XX	AC	ADA08542;	
XX	DT	06-NOV-2003 (first entry)	
XX	DE	Human ovarian carcinoma antigen O772P #2.	
XX	KW	human; gene therapy; ovarian cancer; cancer.	
XX	OS	Homo sapiens.	
XX			

PN	US2003091580-A1.
XX	
PD	15-MAY-2003.
XX	
PF	17-JUL-2001; 2001US-00907969.
XX	
PR	18-JUN-2001; 2001US-00884441.
XX	
PA	(MITC/) MITCHAM J L.
PA	(KING/) KING G E.
PA	(ALGA/) ALGATE P A.
PA	(FLIN/) FLING S P.
PA	(RETT/) RETTER M W.
PA	(FANG/) FANGER G R.
PA	(REED/) REED S G.
PA	(VEDV/) VEDVICK T S.
PA	(CART/) CARTER D.
PA	(HILL/) HILL P.
PA	(ALBO/) ALBONE E.
XX	
PI	Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI	Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX	
DR	WPI; 2003-532352/50.
XX	
PT	New isolated 0772P polypeptides and polynucleotides, useful in gene
PT	therapy, particularly for treating or diagnosing cancer, e.g. ovarian
PT	cancer.
XX	
PS	Example 2; SEQ ID NO 389; 37lpp; English.
XX	
CC	The invention relates to an isolated 0772P polypeptide, which has the
CC	structure fully defined in the specification. The composition containing
CC	the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
CC	or antigen presenting cells are useful for stimulating an immune response
CC	and treating ovarian cancer. Detecting the presence of the
CC	polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
CC	carcinoma cDNAs and protein cDNAs were identified using microarray
CC	technology. The present sequence represents a human ovarian carcinoma
CC	antigen.
XX	
SQ	Sequence 833 AA;
Query Match	100.0%; Score 2321; DB 7; Length 833;
Best Local Similarity	100.0%; Pred. No. 4e-212;
Matches 439; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 FTHRSSVSTTPTGCTPVYLGASKTPASIFGPSAASHLLILFLNFTITNLRYEENMWPG 60
DB	78 FTHRSSVSTTPTGCTPVYLGASKTPASIFGPSAASHLLILFLNFTITNLRYEENMWPG 137
QY	61 SRKNTTERTVLQGLLRPLEKFTSVGLYSGCRLTLRLRPEKGEATGVDAICTHRPDPTGP 120
DB	138 SRKNTTERTVLQGLLRPLEKFTSVGLYSGCRLTLRLRPEKGEATGVDAICTHRPDPTGP 197
QY	121 GLDREQLYLELSQLTHTSITELGPTVTLDRDLSLVNGFTHRSSVPTTSTGWSVEEPTFLNFT 180
DB	198 GLDREQLYLELSQLTHTSITELGPTVTLDRDLSLVNGFTHRSSVPTTSTGWSVEEPTFLNFT 257
QY	181 INNLRYADMGPQSGSLKFNITDNVWKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR 240

DB	258 INNLRYADMGPQSGSLKFNITDNVWKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR 317
QY	241 VDLICTYTLQPLSGPLPIKQVFEHLSQOQTHGTRIGLPYSLDKDSLYLNGYNEPGDPPEPT 300
DB	318 VDLICTYTLQPLSGPLPIKQVFEHLSQOQTHGTRIGLPYSLDKDSLYLNGYNEPGDPPEPT 377
QY	301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMKGKSATFNSTEGVLQHLRL 360
DB	378 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMKGKSATFNSTEGVLQHLRL 437
QY	361 PLFKQSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQQLYWELSOLTH 420
DB	438 PLFKQSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQQLYWELSOLTH 497
QY	421 GVTOLGFYVLDRODSLIFNG 439
DB	498 GVTOLGFYVLDRODSLIFNG 516
RESULT 12	
ADF08885	
ID	ADF08885 standard; protein; 833 AA.
XX	
AC	ADF08885;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Secreted ovarian carcinoma antigen seqid 389.
XX	
KW	gene therapy; protein therapy; vaccine; antibody inhibition;
KW	breast cancer; restorative therapy; diagnostic agent; immunoassay;
KW	secreted ovarian carcinoma antigen.
OS	Homo sapiens.
XX	
PN	US2003124140-A1.
XX	
PD	03-JUL-2003.
XX	
PF	17-JUL-2002; 2002US-00198053.
XX	
PR	17-DEC-1998; 98US-00215681.
PR	17-DEC-1998; 98US-00216003.
PR	23-JUN-1999; 99US-00338933.
PR	24-SEP-1999; 99US-00404879.
PR	17-JUL-2000; 2000US-00617747.
PR	10-AUG-2000; 2000US-00636801.
PR	20-SEP-2000; 2000US-00667857.
PR	04-APR-2001; 2001US-00827271.
PR	18-JUN-2001; 2001US-00884441.
PR	17-JUL-2001; 2001US-00907969.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Bangur CS, Retter MW, Fanger GR, Hill P;
XX	
DR	WPI; 2003-897152/82.
DR	N-PSDB; ADF08882.
XX	
PT	Oncogenic nucleic acids useful for the prevention, diagnosis and
PT	treatment of breast cancer.

XX PS Example 2; SEQ ID NO 389; 399pp; English.

XX The invention describes nucleic acids (I) and the polypeptides (II) they

CC encode. The nucleic acids (I) may be used for preventing, diagnosing and

CC treating diseases related to their aberrant expression i.e. breast

CC cancers. For example, (I) and (II) may be used to treat disorders

CC associated with decreased expression by rectifying mutations or deletions

CC in a patient's genome that affect the activity of (II) by expressing

CC inactive proteins or to supplement the patients own production of (II).

CC Additionally, (I) may be used to produce (III), by inserting (I) into a

CC host cell and culturing the cell to express the protein (II). (I) And its

CC complementary sequences may also be used as DNA probes in diagnostic

CC assays to detect and quantitate the presence of similar nucleic acids in

CC samples, and therefore which patients may be in need of restorative

CC therapy. The host cell may also be used as antigens in the production of

CC antibodies against (II) and in assays to identify modulators of (II)'s

CC expression and activity. The anti-(II) antibodies, agonists and

CC antagonists may be used to regulate expression and activity and as

CC diagnostic agents for detecting the presence of (II) in samples (e.g. by

CC immunoassay). This sequence represents a secreted ovarian carcinoma

CC antigen.

XX SQ Sequence 833 AA;

Query Match 100.0%; Score 2321; DB 7; Length 833;

Best Local Similarity 100.0%; Pred. No. 4e-212;

Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGSPSAASHLLILFTLNFTITNLRYEENWMPG 60

DB 78 FTHRSSVSTTSGTPTVYLGASKTPASIFGSPSAASHLLILFTLNFTITNLRYEENWMPG 137

QY 61 SRKFNTERVLOGLLRPLFKNTSGVLYSGCRLTLRPEKDGATGVDAICTHRDPDTPG 120

DB 138 SRKFNTERVLOGLLRPLFKNTSGVLYSGCRLTLRPEKDGATGVDAICTHRDPDTPG 197

QY 121 GLDEQLYLELSQTHSITHELGPYTLDRSLYVNGFTHRSSVPTTSTGVVSEPTLNFT 180

DB 198 GLDEQLYLELSQTHSITHELGPYTLDRSLYVNGFTHRSSVPTTSTGVVSEPTLNFT 257

QY 181 INNLRYADMCGQSGSLKFNITDNVMKHLSPFLFORSSLGARYTCGRVIALRSVKNGAETR 240

DB 258 INNLRYADMCGQSGSLKFNITDNVMKHLSPFLFORSSLGARYTCGRVIALRSVKNGAETR 317

QY 241 VDLICTYLPQLSGFGLPIKQVFHELSQOQTHGITRLGYSIDKDSLXLNGYNFPGDEPPT 300

DB 318 VDLICTYLPQLSGFGLPIKQVFHELSQOQTHGITRLGYSIDKDSLXLNGYNFPGDEPPT 377

QY 301 TPKPATTELPPLSEATTANGVHLKTLTLNFTISNLQVSPDMKGSAFTNSTGVLOHLR 360

DB 378 TPKPATTELPPLSEATTANGVHLKTLTLNFTISNLQVSPDMKGSAFTNSTGVLOHLR 437

QY 361 PLFOKSSMGPPYLGCOLISLRAPEKGAATGVDTTCTYHPDPVPGCLDIQOLYWELSQLTH 420

DB 438 PLFOKSSMGPPYLGCOLISLRAPEKGAATGVDTTCTYHPDPVPGCLDIQOLYWELSQLTH 497

QY 421 GVTQLGFYVLDROLSLFG 439

DB 498 GVTQLGFYVLDROLSLFG 516

RESULT 13

ADG46172

ID ADG46172 standard; protein; 833 AA.

XX

AC ADG46172;

XX

DT 26-FEB-2004 (first entry)

XX

DE Human ovarian carcinoma polypeptide #3.

XX

KW Human; ovarian carcinoma; O8E; ovarian cancer; secreted tumour antigen;

KW cytostatic; O772P.

XX

OS Homo sapiens.

XX

PN US2003165504-A1.

XX

PD 04-SEP-2003.

XX

PF 04-APR-2001; 2001US-00827271.

XX

PR 17-DEC-1998; 98US-00215681.

PR 17-DEC-1998; 98US-00216003.

PR 23-JUN-1999; 99US-00338933.

PR 24-SEP-1999; 99US-00404879.

PR 17-JUL-2000; 2000US-00617747.

PR 10-AUG-2000; 2000US-00636801.

PR 20-SEP-2000; 2000US-00667857.

XX

PA (RETT/) RETTER M W.

PA (FANG/) FANGER G R.

XX

PI Retter MW, Fanger GR;

XX

DR WPI; 2003-898035/82.

XX

PT New isolated O8E or O772P polypeptides, useful for diagnosing,

PT preventing, treating and monitoring cancer, e.g. ovarian cancer,

PT stimulating the immune response in patient.

XX

PS Claim 5; SEQ ID NO 389; 290pp; English.

XX

CC The invention relates to human ovarian carcinoma polypeptides, designated

CC O8E or O772P, and the polynucleotides encoding them. The invention also

CC relates to methods for inhibiting the development of cancer, e.g. ovarian

CC cancer in a patient, methods for stimulating and/or expanding T cells and

CC methods for identifying secreted tumour antigens. The polypeptides, for

CC compositions, antibodies to the polypeptides and methods are useful for

CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian

CC cancer. The composition is particularly useful for stimulating an immune

CC response in patient. This sequence represents a human ovarian carcinoma

CC polypeptide of the invention.

XX

SQ Sequence 833 AA;

Query Match 100.0%; Score 2321; DB 7; Length 833;

Best Local Similarity 100.0%; Pred. No. 4e-212;

Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGSPSAASHLLILFTLNFTITNLRYEENWMPG 60

Db	78	FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG	137
Qy	61	SRKFNTERVVLQGLLRPLFKNTSGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP	120
Db	138	SRKFNTERVVLQGLLRPLFKNTSGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP	197
Qy	121	GLDREQLYLELSQLSHITELGPYTLDRDSLYVNGFTHRSSVPTTSTGCWSEEPFTLNFT	180
Db	198	GLDREQLYLELSQLSHITELGPYTLDRDSLYVNGFTHRSSVPTTSTGCWSEEPFTLNFT	257
Qy	181	INNLRYMADMGQPSGLKFNITDNVKKHLLSPLFQRSSLGARYTCGRVIALRSVKNGAETR	240
Db	258	INNLRYMADMGQPSGLKFNITDNVKKHLLSPLFQRSSLGARYTCGRVIALRSVKNGAETR	317
Qy	241	VOLLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPLYSLDKDSLXLNGYNEPGDPPT	300
Db	318	VOLLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPLYSLDKDSLXLNGYNEPGDPPT	377
Qy	301	TPKPATTFPLPULSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATNSTEGVLQHLR	360
Db	378	TPKPATTFPLPULSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATNSTEGVLQHLR	437
Qy	361	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQQLYWELSOLTH	420
Db	438	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQQLYWELSOLTH	497
Qy	421	GVTQLGFYVLDKDSLFLNG	439
Db	498	GVTQLGFYVLDKDSLFLNG	516
Qy	421	GVTQLGFYVLDKDSLFLNG	439
Db	498	GVTQLGFYVLDKDSLFLNG	516
RESULT 14			
ADX17768			
ID	ADX17768	standard; protein; 833 AA.	
XX	ADX17768;		
XX			
DT	21-APR-2005	(first entry)	
DE	Human ovarian carcinoma antigen cDNA 0772P clone 21003 encoded protein.		
XX			
KW	diagnosis; cytostatic; immunostimulant; gene therapy; tumor;		
XX	ovarian tumor; cancer; carcinoma; antigen.		
OS	Homo sapiens.		
XX			
PN	US2005031634-A1.		
XX			
PD	10-FEB-2005.		
XX			
PF	02-JUN-2004; 2004US-00860790.		
XX			
PR	17-DEC-1998; 98US-00216003.		
PR	23-JUN-1999; 99US-00338933.		
PR	24-SEP-1999; 99US-00404879.		
PR	17-JUL-2000; 2000US-00617747.		
PR	10-AUG-2000; 2000US-00636801.		
PR	20-SEP-2000; 2000US-00667857.		
PR	04-APR-2001; 2001US-00827271.		
PR	18-JUN-2001; 2001US-00884441.		

PR	17-JUL-2001; 2001US-00907969.		
PR	17-JUL-2002; 2002US-00198053.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Bangur CS, Retter MW, Fanger GR, Hill P;		
XX			
DR	WPI; 2005-151645/16.		
XX			
PT	New ovarian carcinoma polynucleotides, preferably cDNAs, useful for		
PT	diagnosing, preventing and treating diseases, such as ovarian cancer, and		
PT	for eliciting humoral and/or cellular immune response.		
XX			
PS	Example 2; SEQ ID NO 389; 398pp; English.		
XX			
CC	The invention relates to an isolated polynucleotide comprising a sequence		
CC	of, a sequence hybridizing under highly stringent conditions to, or		
CC	having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in		
CC	the specification, its complement or degenerate variants, or a sequence		
CC	of at least 20 contiguous residues of the 849 or 1399 bp sequence. The		
CC	polynucleotides and polypeptides are useful for diagnosing, preventing		
CC	and treating diseases, such as ovarian cancer, and for eliciting humoral		
CC	and/or cellular immune response. This sequence corresponds to an ovarian		
CC	carcinoma antigen protein of the invention.		
XX			
SQ	Sequence 833 AA;		
	Query Match 100.0%; Score 2321; DB 9; Length 833;		
	Best Local Similarity 100.0%; Pred. No. 4e-212;		
	Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG	60
Db	78	FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG	137
Qy	61	SRKFNTERVVLQGLLRPLFKNTSGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP	120
Db	138	SRKFNTERVVLQGLLRPLFKNTSGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP	197
Qy	121	GLDREQLYLELSQLSHITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVSEEPFTLNFT	180
Db	198	GLDREQLYLELSQLSHITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVSEEPFTLNFT	257
Qy	181	INNLRYMADMGQPSGLKFNITDNVKKHLLSPLFQRSSLGARYTCGRVIALRSVKNGAETR	240
Db	258	INNLRYMADMGQPSGLKFNITDNVKKHLLSPLFQRSSLGARYTCGRVIALRSVKNGAETR	317
Qy	241	VOLLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPLYSLDKDSLXLNGYNEPGDPPT	300
Db	318	VOLLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPLYSLDKDSLXLNGYNEPGDPPT	377
Qy	301	TPKPATTFPLPULSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR	360
Db	378	TPKPATTFPLPULSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR	437
Qy	361	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQQLYWELSOLTH	420
Db	438	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQQLYWELSOLTH	497
Qy	421	GVTQLGFYVLDKDSLFLNG	439

Db 498 GVTQLGFYVLDROSLFING 516

RESULT 15  
AAB12552  
ID AAB12552 standard; protein; 914 AA.  
XX AC AAB12552;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:312.  
XX  
KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;  
KW tumour antigen; identification; cytostatic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN W0200036107-A2.  
XX  
PD 22-JUN-2000.  
XX  
PF 17-DEC-1999; 99WO-US030270.  
XX  
PR 17-DEC-1998; 98US-00215681.  
PR 17-DEC-1998; 98US-00216003.  
PR 23-JUN-1999; 99US-00338933.  
PR 24-SEP-1999; 99US-00404879.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Mitcham JL, King GE, Algate PA, Frudakis TN;  
XX  
DR WPI: 2000-431589/37.  
DR N-PSDB; AAA70001.  
XX  
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid  
PT encoding it, useful for the diagnosis, prevention and treatment of  
PT cancer, preferably ovarian cancer.  
XX  
PS Example 2; Page 172-174; 299pp; English.  
XX  
CC The present invention describes an isolated polypeptide comprising an  
CC immunogenic portion of an ovarian carcinoma protein (or its variants).  
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have  
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian  
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful  
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian  
CC cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human  
CC ovarian carcinoma polynucleotides and proteins used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 914 AA;

Query Match 100.0%; Score 2321; DB 3; Length 914;  
Best Local Similarity 100.0%; Pred. No. 4.6e-212;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 159 FTHRSSVSTTGTCTPVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218

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|||||  
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRLPEKDGATGVDAICTHRPDPGTP 278  
|||||  
QY 121 GLDREQLYLELSQLTHSITELGPTYTLDRDSLXVNGFTHRSSVPTTSTGCVSEEPFTLNFT 180  
|||||  
Db 279 GLDREQLYLELSQLTHSITELGPTYTLDRDSLXVNGFTHRSSVPTTSTGCVSEEPFTLNFT 338  
|||||  
QY 181 INNLRYMADWGQPGSLKFNTDNVWKHLSPLFQSSIGARYTGCRVIALRSVKNGAETR 240  
|||||  
Db 339 INNLRYMADWGQPGSLKFNTDNVWKHLSPLFQSSIGARYTGCRVIALRSVKNGAETR 398  
|||||  
QY 241 VDLCTYLOPLSGPGLPIKQVFHELSSQOOTHGTRGLGYPYSLDKDSLXLNGYNRPDEPPT 300  
|||||  
Db 399 VDLCTYLOPLSGPGLPIKQVFHELSSQOOTHGTRGLGYPYSLDKDSLXLNGYNRPDEPPT 458  
|||||  
QY 301 TPKPATTELPPLSEATTAMGYHLKTLTLNFTISNLOQSPDMGKGSATENSTEGVLOHLR 360  
|||||  
Db 459 TPKPATTELPPLSEATTAMGYHLKTLTLNFTISNLOQSPDMGKGSATENSTEGVLOHLR 518  
|||||  
QY 361 PLFQKSSMGPFYLGQQLISLRPEKDGAAATGVDTCTTYHPDPVPGGLDIQQLYWELSQLTH 420  
|||||  
Db 519 PLFQKSSMGPFYLGQQLISLRPEKDGAAATGVDTCTTYHPDPVPGGLDIQQLYWELSQLTH 578  
|||||  
QY 421 GVTQLGFYVLDROSLFING 439  
|||||  
Db 579 GVTQLGFYVLDROSLFING 597

Search completed: June 7, 2007, 17:52:44  
Job time : 215 secs

SCORE 2.0 BuildDate: 12/05/2005

**SCORE Search Results Details for Application  
10687035 and Search Result  
20070607\_154741\_us-10-687-035-  
1\_copy\_14\_452.rai.**

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OM protein - protein search, using sw model

Run on: June 7, 2007, 17:51:47 ; Search time 115 Seconds  
(without alignments)  
334.139 Million cell updates/sec

Title: US-10-687-035-1\_COPY\_14\_452  
Perfect score: 2321  
Sequence: 1 FTHRSSVSTTGTGTPTVY.....HGVTLGFYVLDROSLFNG 439

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /EMC\_Celerra\_SiDS3/ptodata/2/iaa/5\_COMB.pep.\*  
2: /EMC\_Celerra\_SiDS3/ptodata/2/iaa/6\_COMB.pep.\*  
3: /EMC\_Celerra\_SiDS3/ptodata/2/iaa/7\_COMB.pep.\*  
4: /EMC\_Celerra\_SiDS3/ptodata/2/iaa/H\_COMB.pep.\*  
5: /EMC\_Celerra\_SiDS3/ptodata/2/iaa/PTUS\_COMB.pep.\*  
6: /EMC\_Celerra\_SiDS3/ptodata/2/iaa/RE\_COMB.pep.\*  
7: /EMC\_Celerra\_SiDS3/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2321	100.0	772	2	US-09-404-879A-388	Sequence 388, App
2	2321	100.0	772	2	US-09-667-857-388	Sequence 388, App
3	2321	100.0	772	2	US-10-198-053-388	Sequence 388, App
4	2321	100.0	772	2	US-09-827-271-388	Sequence 388, App
5	2321	100.0	833	2	US-09-404-879A-389	Sequence 389, App
6	2321	100.0	833	2	US-09-667-857-389	Sequence 389, App
7	2321	100.0	833	2	US-10-198-053-389	Sequence 389, App
8	2321	100.0	833	2	US-09-827-271-389	Sequence 389, App
9	2321	100.0	914	2	US-09-404-879A-312	Sequence 312, App
10	2321	100.0	914	2	US-09-338-933-312	Sequence 312, App
11	2321	100.0	914	2	US-09-667-857-312	Sequence 312, App
12	2321	100.0	914	2	US-10-198-053-312	Sequence 312, App
13	2321	100.0	914	2	US-10-198-053-478	Sequence 478, App
14	2321	100.0	914	2	US-09-827-271-312	Sequence 312, App
15	2312	99.6	3451	2	US-10-198-053-595	Sequence 595, App
16	2301	99.1	1148	2	US-10-198-053-458	Sequence 458, App
17	2301	99.1	1148	2	US-10-198-053-479	Sequence 479, App
18	2301	99.1	1148	2	US-09-827-271-458	Sequence 458, App
19	2301	99.1	1156	2	US-10-198-053-459	Sequence 459, App
20	2301	99.1	1156	2	US-09-827-271-459	Sequence 459, App
21	1436	61.9	304	2	US-10-198-053-486	Sequence 486, App
22	842.5	36.3	294	2	US-10-198-053-487	Sequence 487, App
23	814	35.1	313	2	US-10-198-053-461	Sequence 461, App
24	814	35.1	313	2	US-09-827-271-461	Sequence 461, App
25	809	34.9	155	2	US-10-198-053-591	Sequence 591, App
26	800	34.5	150	2	US-10-198-053-593	Sequence 593, App
27	697	30.0	134	2	US-10-198-053-592	Sequence 592, App
28	675.5	28.1	210	2	US-10-198-053-481	Sequence 481, App
29	662	28.5	230	2	US-10-198-053-480	Sequence 480, App
30	659.5	28.4	156	2	US-10-198-053-589	Sequence 589, App
31	651.5	28.1	156	2	US-10-198-053-596	Sequence 596, App
32	648	27.9	438	2	US-09-404-879A-390	Sequence 390, App
33	648	27.9	438	2	US-09-667-857-390	Sequence 390, App
34	648	27.9	438	2	US-10-198-053-390	Sequence 390, App
35	648	27.9	438	2	US-10-198-053-483	Sequence 483, App
36	648	27.9	438	2	US-09-827-271-390	Sequence 390, App
37	637.5	27.5	156	2	US-10-198-053-590	Sequence 590, App
38	611.5	26.3	268	2	US-10-198-053-485	Sequence 485, App
39	607.5	26.2	156	2	US-10-198-053-584	Sequence 584, App
40	600.5	25.9	156	2	US-10-198-053-587	Sequence 587, App
41	599.5	25.8	156	2	US-10-198-053-583	Sequence 583, App
42	598.5	25.8	156	2	US-10-198-053-586	Sequence 586, App
43	595.5	25.7	156	2	US-10-198-053-588	Sequence 588, App
44	592.5	25.5	156	2	US-10-198-053-580	Sequence 580, App
45	589.5	25.4	156	2	US-10-198-053-577	Sequence 577, App

ALIGNMENTS

RESULT 1  
US-09-404-879A-388  
; Sequence 388, Application US/09404879A  
; Patent No. 6468546  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.

```
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-879A-388

Query Match      100.0%; Score 2321; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLYEENWMPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLYEENWMPG 218

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 278

Qy 121 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

Qy 181 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARTGCRVIALRSVKNGAETR 240
Db 339 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARTGCRVIALRSVKNGAETR 398

Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGPLYSLDKDSLYLNGYNERPDPPT 300
Db 399 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGPLYSLDKDSLYLNGYNERPDPPT 458

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Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLYQSPDMKGSAFNSTEGVLOHLR 518

Qy 361 PLFKSSKGPFFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGCLDIQOLYWELSOLTH 420
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Qy 421 GVTOLGFVLDROSLFING 439
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RESULT 2
US-09-667-857-388
; Sequence 388, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
```

```
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-667-857-388
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Query Match      100.0%; Score 2321; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLYEENWMPG 218

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 278

Qy 121 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

Qy 181 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARTGCRVIALRSVKNGAETR 240
Db 339 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARTGCRVIALRSVKNGAETR 398

Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGPLYSLDKDSLYLNGYNERPDPPT 300
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Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLYQSPDMKGSAFNSTEGVLOHLR 360
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLYQSPDMKGSAFNSTEGVLOHLR 518

Qy 361 PLFKSSKGPFFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGCLDIQOLYWELSOLTH 420
Db 519 PLFKSSKGPFFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGCLDIQOLYWELSOLTH 578

Qy 421 GVTOLGFVLDROSLFING 439
Db 579 GVTOLGFVLDROSLFING 597
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RESULT 3
US-10-198-053-388
; Sequence 388, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
```

```
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-388

Query Match      100.0%; Score 2321; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 339 INNLRYWADMGQPSGLKFNITDNVWKHLLSPLFORSSLGARYTCGRVIALRSVKNGAETR 398
Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQOTHGITRLGPLYSLDKDSLYLNGYNEPGDPPT 300
Db 399 VDLCTYLOPLSGPLPIKQVFHELSSQOTHGITRLGPLYSLDKDSLYLNGYNEPGDPPT 458
Qy 301 TKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 360
Db 459 TKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 518
Qy 361 PLFQKSSMGFFYLGCOLISURPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSQLTH 420
Db 519 PLFQKSSMGFFYLGCOLISURPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSQLTH 578
Qy 421 GVTQLGFFYVLDRLDSLIFNG 439
Db 579 GVTQLGFFYVLDRLDSLIFNG 597

RESULT 4
US-09-827-271-388
; Sequence 388, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
```

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; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-388

Query Match      100.0%; Score 2321; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
Db 159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPG 120
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPG 278
Qy 121 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 338
Qy 181 INNLRYWADMGQPSGLKFNITDNVWKHLLSPLFORSSLGARYTCGRVIALRSVKNGAETR 240
Db 339 INNLRYWADMGQPSGLKFNITDNVWKHLLSPLFORSSLGARYTCGRVIALRSVKNGAETR 398
Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQOTHGITRLGPLYSLDKDSLYLNGYNEPGDPPT 300
Db 399 VDLCTYLOPLSGPLPIKQVFHELSSQOTHGITRLGPLYSLDKDSLYLNGYNEPGDPPT 458
Qy 301 TKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 360
Db 459 TKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 518
Qy 361 PLFQKSSMGFFYLGCOLISURPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSQLTH 420
Db 519 PLFQKSSMGFFYLGCOLISURPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSQLTH 578
Qy 421 GVTQLGFFYVLDRLDSLIFNG 439
Db 579 GVTQLGFFYVLDRLDSLIFNG 597

RESULT 5
US-09-404-879A-389
; Sequence 389, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
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; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-879A-389

Query Match      100.0%; Score 2321; DB 2; Length 833;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||
Db 78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
    |||||||
Db 138 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 197

Qy 121 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||||||
Db 198 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257

Qy 181 INNLRYADMGGPSLKFNITDNVWKHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 240
    |||||||
Db 258 INNLRYADMGGPSLKFNITDNVWKHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 317

Qy 241 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPCGDEPPT 300
    |||||||
Db 318 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPCGDEPPT 377

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 360
    |||||||
Db 378 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 437

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
    |||||||
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 497

Qy 421 GVTOLGFYVLDSDLSLFG 439
    |||||||
Db 498 GVTOLGFYVLDSDLSLFG 516

RESULT 6
US-09-667-857-389
; Sequence 389, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
```

```
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-667-857-389

Query Match      100.0%; Score 2321; DB 2; Length 833;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||
Db 78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
    |||||||
Db 138 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 197

Qy 121 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||||||
Db 198 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257

Qy 181 INNLRYADMGGPSLKFNITDNVWKHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 240
    |||||||
Db 258 INNLRYADMGGPSLKFNITDNVWKHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 317

Qy 241 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPCGDEPPT 300
    |||||||
Db 318 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPCGDEPPT 377

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 360
    |||||||
Db 378 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 437

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
    |||||||
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 497

Qy 421 GVTOLGFYVLDSDLSLFG 439
    |||||||
Db 498 GVTOLGFYVLDSDLSLFG 516

RESULT 7
US-10-198-053-389
; Sequence 389, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
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; CURRENT FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 624  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 389  
; LENGTH: 833  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-198-053-389

Query Match 100.0%; Score 2321; DB 2; Length 833;  
Best Local Similarity 100.0%; Pred. No. 1.1e-222;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60  
Db FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137  
  
Qy 61 SRKFNTERVVOGLLRPLFKNTSVGPLYSGCRUTLLRPEKDGATGVDAICTHRPDTGP 120  
Db SRKFNTERVVOGLLRPLFKNTSVGPLYSGCRUTLLRPEKDGATGVDAICTHRPDTGP 197  
  
Qy 121 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 180  
Db GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 257  
  
Qy 181 INNLRYWADMGGPGLSKFNITDNVWKHLLSPLFORSSIGARYTGCRAIALRSVKNGAETR 240  
Db INNLRYWADMGGPGLSKFNITDNVWKHLLSPLFORSSIGARYTGCRAIALRSVKNGAETR 317  
  
Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPLYSLDKDSLYLNGYNEPGDEPPT 300  
Db VDLCTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPLYSLDKDSLYLNGYNEPGDEPPT 377  
  
Qy 301 TPKPATTFLLPPLSEATTAMGYHLKTLTUNFTISNLOYSQPMGKGSATFNSTEGVLOHLLR 360  
Db TPKPATTFLLPPLSEATTAMGYHLKTLTUNFTISNLOYSQPMGKGSATFNSTEGVLOHLLR 437  
  
Qy 361 PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 420  
Db PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 497  
  
Qy 421 GVTQLGFYVLDRLDSLFING 439  
Db GVTQLGFYVLDRLDSLFING 516

RESULT 8  
US-09-827-271-389  
; Sequence 389, Application US/09827271  
; Patent No. 6962980  
; GENERAL INFORMATION:  
; APPLICANT: Retter, Gary R.  
; APPLICANT: Fanger, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C6  
; CURRENT APPLICATION NUMBER: US/09/827,271  
; CURRENT FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 389

; LENGTH: 833  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-827-271-389

Query Match 100.0%; Score 2321; DB 2; Length 833;  
Best Local Similarity 100.0%; Pred. No. 1.1e-222;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60  
Db FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137  
  
Qy 61 SRKFNTERVVOGLLRPLFKNTSVGPLYSGCRUTLLRPEKDGATGVDAICTHRPDTGP 120  
Db SRKFNTERVVOGLLRPLFKNTSVGPLYSGCRUTLLRPEKDGATGVDAICTHRPDTGP 197  
  
Qy 121 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 180  
Db GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 257  
  
Qy 181 INNLRYWADMGGPGLSKFNITDNVWKHLLSPLFORSSIGARYTGCRAIALRSVKNGAETR 240  
Db INNLRYWADMGGPGLSKFNITDNVWKHLLSPLFORSSIGARYTGCRAIALRSVKNGAETR 317  
  
Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPLYSLDKDSLYLNGYNEPGDEPPT 300  
Db VDLCTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPLYSLDKDSLYLNGYNEPGDEPPT 377  
  
Qy 301 TPKPATTFLLPPLSEATTAMGYHLKTLTUNFTISNLOYSQPMGKGSATFNSTEGVLOHLLR 360  
Db TPKPATTFLLPPLSEATTAMGYHLKTLTUNFTISNLOYSQPMGKGSATFNSTEGVLOHLLR 437  
  
Qy 361 PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 420  
Db PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 497  
  
Qy 421 GVTQLGFYVLDRLDSLFING 439  
Db GVTQLGFYVLDRLDSLFING 516

RESULT 9  
US-09-404-879A-312  
; Sequence 312, Application US/09404879A  
; Patent No. 6468546  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Algate, Paul A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C2  
; CURRENT APPLICATION NUMBER: US/09/404,879A  
; CURRENT FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 393  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 312  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Homo sapien

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US-09-404-879A-312

Query Match      100.0%; Score 2321; DB 2; Length 914;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTPTGTPFVVLGASKTTPASIFGSPAASHLLILFTLNFTTNLRYYENWMPG 60
    |||||
Db 159 FTHRSSVSTTPTGTPFVVLGASKTTPASIFGSPAASHLLILFTLNFTTNLRYYENWMPG 218
    |||||

Qy 61 SRKFNTTVERVLOGLLRPLFKNTSGPLYSGCRLTLIRPEKDEATGVDAICTHRPDPFGP 120
    |||||
Db 219 SRKFNTTVERVLOGLLRPLFKNTSGPLYSGCRLTLIRPEKDEATGVDAICTHRPDPFGP 278
    |||||

Qy 121 GLDREQLYLELSQLTHSIFELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||||
Db 279 GLDREQLYLELSQLTHSIFELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
    |||||

Qy 181 INNLRYMADMGQPSGLKFNTIDTNMKHLLSPLFQRSSLGARTGCRVIALRSVKNGAETR 240
    |||||
Db 339 INNLRYMADMGQPSGLKFNTIDTNMKHLLSPLFQRSSLGARTGCRVIALRSVKNGAETR 398
    |||||

Qy 241 VDLCTTYLOPLSGPLPIKQVFEHLSQOOTHGITRGLGPISLDKDSLYLYNGYNPGDEPPT 300
    |||||
Db 399 VDLCTTYLOPLSGPLPIKQVFEHLSQOOTHGITRGLGPISLDKDSLYLYNGYNPGDEPPT 458
    |||||

Qy 301 TPKPATTFLPPLSEATTAKGYHLKATLTNFTLSNLQYSPDMGKGSATFNSTEGVLQHLR 360
    |||||
Db 459 TPKPATTFLPPLSEATTAKGYHLKATLTNFTLSNLQYSPDMGKGSATFNSTEGVLQHLR 518
    |||||

Qy 361 PLFQKSMGPFYLGCOLISLRPKDGAATGVDTTCTTYPDPVPGPLDIQQLWELSQLTH 420
    |||||
Db 519 PLFQKSMGPFYLGCOLISLRPKDGAATGVDTTCTTYPDPVPGPLDIQQLWELSQLTH 578
    |||||

Qy 421 GVTQLGYVLDROSLFNG 439
    |||||
Db 579 GVTQLGYVLDROSLFNG 597

RESULT 10
US-09-338-933-312
; Sequence 312, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-338-933-312

Query Match      100.0%; Score 2321; DB 2; Length 914;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;

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	Matches	439;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
Qy	1	FTHRSSVSTTSGTPTTVYLGASKTPASIFGSAASHLLILFLTNFTITNLAYEENMMPG	60						
Dd	159	FTHRSSVSTTSGTPTTVYLGASKTPASIFGSAASHLLILFLTNFTITNLAYEENMMPG	218						
Qy	61	SRKENTERVLOGLRLPLFKNTSVGPYLSGCRUTLLRPEKDGEATGVDAICTHRPDTGP	120						
Dd	219	SRKENTERVLOGLRLPLFKNTSVGPYLSGCRUTLLRPEKDGEATGVDAICTHRPDTGP	278						
Qy	121	GLDRQLYLLELSQLTSHSTELGPYTLDRDSLRYNGFTHRSSVPPTSTGCVSEEPFTLNFT	180						
Dd	279	GLDRQLYLLELSQLTSHSTELGPYTLDRDSLRYNGFTHRSSVPPTSTGCVSEEPFTLNFT	338						
Qy	181	NNLRYMADMGQGSLKFNTDNVKHLLSPLFQRSSILGARVTGCRVIALLRSVKNGAETR	240						
Dd	339	NNLRYMADMGQGSLKFNTDNVKHLLSPLFQRSSILGARVTGCRVIALLRSVKNGAETR	398						
Qy	241	VDLLCTYLOPSGGLPIKVHFELSQQOTHGITRULGPYSLDKDSLYLNGYNFGPDDEPPT	300						
Dd	399	VDLLCTYLOPSGGLPIKVHFELSQQOTHGITRULGPYSLDKDSLYLNGYNFGPDDEPPT	458						
Qy	301	TKPKATTFLPPLEAETAMGYHLKTILNTINLQVSPDMKGSAFTNSTGVLIQHLLR	360						
Dd	459	TKPKATTFLPPLEAETAMGYHLKTILNTINLQVSPDMKGSAFTNSTGVLIQHLLR	518						
Qy	361	PLPFKSSNGFYLGCLLSLRPEKDGAATGVDTCTVHPDPVPGGLDIOOLYWELSQLTH	420						
Dd	519	PLPFKSSNGFYLGCLLSLRPEKDGAATGVDTCTVHPDPVPGGLDIOOLYWELSQLTH	578						
Qy	421	GVTLQGFYVLDRDSLFG	439						
Dd	579	GVTLQGFYVLDRDSLFG	597						
RESULT	11								
	US-09-667-857-312								
	; Sequence 312, Application US/09667857								
	; Patent No. 6699664								
	; GENERAL INFORMATION:								
	; APPLICANT: Mitcham, Jennifer L.								
	; APPLICANT: King, Gordon E.								
	; APPLICANT: Algate, Paul A.								
	; APPLICANT: Fling, Steven P.								
	; APPLICANT: Retter, Marc W.								
	; APPLICANT: Fanger, Gary Richard								
	; APPLICANT: Reed, Steven G.								
	; APPLICANT: Vedwick, Thomas S.								
	; APPLICANT: Carter, Darrick								
	; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND								
	; FILE REFERENCE: 210121.462C5								
	; CURRENT APPLICATION NUMBER: US/09/667,857								
	; CURRENT FILING DATE: 2000-09-20								
	; NUMBER OF SEQ ID NOS: 455								
	; SOFTWARE: FastSeq for Windows Version 3.0								
	; SEQ ID NO 312								
	; LENGTH: 914								
	; TYPE: PRT								
	; ORGANISM: Homo sapien								
	US-09-667-857-312								

Query Match									
Best Local Similarity 100.0%; Score 2321; DB 2; Length 914;									
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	FTHRSSVSTTSGTPTTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG	60						
Db	159	FTHRSSVSTTSGTPTTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG	218						
Qy	61	SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGATGDAICTHRPDPTGP	120						
Db	219	SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGATGDAICTHRPDPTGP	278						
Qy	121	GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT	180						
Db	279	GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT	338						
Qy	181	INNLRYMADMGQPSLKFENITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNGAETR	240						
Db	339	INNLRYMADMGQPSLKFENITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNGAETR	398						
Qy	241	VOLLCTVLOPLSGPLPIKOVFHELSSQTHGITRLGYPYSLDKDSLYLNGYNEPGDEPPT	300						
Db	399	VOLLCTVLOPLSGPLPIKOVFHELSSQTHGITRLGYPYSLDKDSLYLNGYNEPGDEPPT	458						
Qy	301	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLOHLRL	360						
Db	459	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLOHLRL	518						
Qy	361	PLFQKSSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH	420						
Db	519	PLFQKSSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH	578						
Qy	421	GVTQLGFVILDRDSLFIING	439						
Db	579	GVTQLGFVILDRDSLFIING	597						
RESULT 12									
US-10-198-053-312									
; Sequence 312 Application US/10198053									
; Patent No. 6858710									
; GENERAL INFORMATION:									
; APPLICANT: Bangur, Chaitanya S.									
; APPLICANT: Retter, Marc W.									
; APPLICANT: Fanger, Gary R.									
; APPLICANT: Hill, Paul									
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY									
; FILE REFERENCE: 210121.462C9									
; CURRENT APPLICATION NUMBER: US/10/198,053									
; CURRENT FILING DATE: 2002-07-17									
; NUMBER OF SEQ ID NOS: 624									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 312									
; LENGTH: 914									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-198-053-312									
Query Match									
100.0%; Score 2321; DB 2; Length 914;									

Best Local Similarity 100.0%; Pred. No. 1.3e-222;									
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	FTHRSSVSTTSGTPTTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG	60						
Db	159	FTHRSSVSTTSGTPTTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG	218						
Qy	61	SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGATGDAICTHRPDPTGP	120						
Db	219	SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGATGDAICTHRPDPTGP	278						
Qy	121	GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT	180						
Db	279	GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT	338						
Qy	181	INNLRYMADMGQPSLKFENITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNGAETR	240						
Db	339	INNLRYMADMGQPSLKFENITDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNGAETR	398						
Qy	241	VOLLCTVLOPLSGPLPIKOVFHELSSQTHGITRLGYPYSLDKDSLYLNGYNEPGDEPPT	300						
Db	399	VOLLCTVLOPLSGPLPIKOVFHELSSQTHGITRLGYPYSLDKDSLYLNGYNEPGDEPPT	458						
Qy	301	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLOHLRL	360						
Db	459	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLOHLRL	518						
Qy	361	PLFQKSSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH	420						
Db	519	PLFQKSSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH	578						
Qy	421	GVTQLGFVILDRDSLFIING	439						
Db	579	GVTQLGFVILDRDSLFIING	597						
RESULT 13									
US-10-198-053-478									
; Sequence 478 Application US/10198053									
; Patent No. 6858710									
; GENERAL INFORMATION:									
; APPLICANT: Bangur, Chaitanya S.									
; APPLICANT: Retter, Marc W.									
; APPLICANT: Fanger, Gary R.									
; APPLICANT: Hill, Paul									
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY									
; FILE REFERENCE: 210121.462C9									
; CURRENT APPLICATION NUMBER: US/10/198,053									
; CURRENT FILING DATE: 2002-07-17									
; NUMBER OF SEQ ID NOS: 624									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 478									
; LENGTH: 914									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-198-053-478									
Query Match									
100.0%; Score 2321; DB 2; Length 914;									
Best Local Similarity 100.0%; Pred. No. 1.3e-222;									
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									

Qy 1 FTHRSSVSTSTGPTGYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60  
Db 159 FTHRSSVSTSTGPTGYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218

Qy 61 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGTP 120  
Db 219 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGTP 278

Qy 121 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
Db 279 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

Qy 181 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRVIALRSVKNGAETR 240  
Db 339 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRVIALRSVKNGAETR 398

Qy 241 VDLCTYIQPLSGPLPIKQVFHELSSQOOTHGITRLGYSLDKDSLXNGYNEPGDEPPT 300  
Db 399 VDLCTYIQPLSGPLPIKQVFHELSSQOOTHGITRLGYSLDKDSLXNGYNEPGDEPPT 458

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 360  
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHHPDPVPGGLDIQOLYWELSLQTH 420  
Db 519 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHHPDPVPGGLDIQOLYWELSLQTH 578

Qy 421 GVTQLGFYVLDROSLFING 439  
Db 579 GVTQLGFYVLDROSLFING 597

RESULT 14  
US-09-827-271-312  
; Sequence 312, Application US/09827271  
; Patent No. 6962980  
; GENERAL INFORMATION:  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.462C6  
; CURRENT APPLICATION NUMBER: US/09/827,271  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 312  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-827-271-312

Query Match 100.0%; Score 2321; DB 2; Length 914;  
Best Local Similarity 100.0%; Pred. No. 1.3e-222;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTGPTGYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60  
Db 159 FTHRSSVSTSTGPTGYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218

Qy 61 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGTP 120  
Db 219 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGTP 278

Qy 121 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
Db 279 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

Qy 181 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRVIALRSVKNGAETR 240  
Db 339 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSLGARYTGCRVIALRSVKNGAETR 398

Qy 241 VDLCTYIQPLSGPLPIKQVFHELSSQOOTHGITRLGYSLDKDSLXNGYNEPGDEPPT 300  
Db 399 VDLCTYIQPLSGPLPIKQVFHELSSQOOTHGITRLGYSLDKDSLXNGYNEPGDEPPT 458

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 360  
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHHPDPVPGGLDIQOLYWELSLQTH 420  
Db 519 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHHPDPVPGGLDIQOLYWELSLQTH 578

Qy 421 GVTQLGFYVLDROSLFING 439  
Db 579 GVTQLGFYVLDROSLFING 597

RESULT 15  
US-10-198-053-595  
; Sequence 595, Application US/10198053  
; Patent No. 6858710  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Hill, Paul  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.462C9  
; CURRENT APPLICATION NUMBER: US/10/198,053  
; CURRENT FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 624  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 595  
; LENGTH: 3451  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 177, 335, 523, 618, 563, 875, 961, 1001, 1441, 1555, 1560,  
; LOCATION: 1563, 1574, 1585, 2065, 2070, 2683, 2990, 3269, 3381, 3401  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-10-198-053-595

Query Match 99.6%; Score 2312; DB 2; Length 3451;  
Best Local Similarity 99.8%; Pred. No. 8.8e-221;  
Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	2696	FTHRSSVSTTGTCTVYLGASKTPASIFGFSAAASHLLILFTLNFTITNLRAYENWMPG	2755
Qy	61	SRKENTTERRVLQGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRDPDTPG	120
Db	2756	SRKENTTERRVLQGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRDPDTPG	2815
Qy	121	GLDREQLYLELSQTHSITELGPTYLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT	180
Db	2816	GLDREQLYLELSQTHSITELGPTYLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT	2875
Qy	181	INNLRVYMDMGQPGSLKFNITDNVMKHLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR	240
Db	2876	INNLRVYMDMGQPGSLKFNITDNVMKHLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR	2935
Qy	241	VDLLCTYLQPLSGGGLPIKQVFHELSCQTHGITRLGPISLDKDSLTVNGYNEPGDEPPT	300
Db	2936	VDLLCTYLQPLSGGGLPIKQVFHELSCQTHGITRLGPISLDKDSLTVNGYNEPGDEPPT	2995
Qy	301	TPKPATTELPPLSEATTANGYHLKTLTLNFTISNLOYSPDMGKGSATFNSTEGVLQHLLR	360
Db	2996	TPKPATTELPPLSEATTANGYHLKTLTLNFTISNLOYSPDMGKGSATFNSTEGVLQHLLR	3055
Qy	361	PLFOKSSMGPFYLGCOLISLRAPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSOLTH	420
Db	3056	PLFOKSSMGPFYLGCOLISLRAPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSOLTH	3115
Qy	421	GVTOGLGVYVLDRODSLFLNG	439
Db	3116	GVTOGLGVYVLDRODSLFLNG	3134

Search completed: June 7, 2007, 17:53:42  
Job time : 115 secs

## SCORE Search Results Details for Application 10687035 and Search Result 20070607\_154735\_us-10-687-035- 1\_copy\_14\_452.rup.

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This page gives you Search Results detail for the Application 10687035 and Search Result 20070607\_154735\_us-10-687-035-1\_copy\_14\_452.rup.

[Go Back to previous page](#)

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: June 7, 2007, 17:45:26 ; Search time 373 Seconds  
(without alignments)  
1261.830 Million cell updates/sec

Title: US-10-687-035-1\_COPY\_14\_452

Perfect score: 2321  
Sequence: 1 FTHRSSVSTSTPGPTVYL.....HGVTLGFVLDRLDSLFING 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues 3281787

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_8.4.:

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2317	99.8	6995	2 Q96RK2_HUMAN	Q96rk2 homo sapien

2	2301	99.1	1148	2	Q9H7S7_HUMAN	Q9h7s7 homo sapien
3	2301	99.1	22152	2	Q8WX17_HUMAN	Q8wx17 homo sapien
4	1512	65.1	867	2	Q6ZQW5_HUMAN	Q6zqw5 homo sapien
5	217	9.3	258	2	Q9D1H1_MOUSE	Q9d1h1 mus musculus
6	117.5	5.1	729	2	Q8DKG0_SYNEL	Q8dkg0 synechococc
7	115.5	5.0	865	2	Q2FND5_METHJ	Q2fnd5 methanospir
8	115	5.0	531	2	Q16X85_AEDAE	Q16x85 aedes aegyp
9	114.5	4.9	1475	1	NUI53_HUMAN	P49790 homo sapien
10	114	4.9	5010	2	Q716A3_9APHY	Q716a3 trametres sp
11	114	4.9	5010	2	Q4MT18_BACCE	Q4mt18 bacillus ce
12	113.5	4.9	1386	2	Q6P5E2_MOUSE	Q6p5e2 mus musculu
13	113	4.9	520	2	Q716A2_9APHY	Q716a2 trametres sp
14	113	4.9	3486	2	Q28LC2_JANSC	Q28lc2 jannaschia
15	112.5	4.8	1625	2	Q6MVD4_NEUCR	Q6mvd4 neuropept
16	112	4.8	1346	2	Q6ZQ24_MOUSE	Q6zq24 mus musculu
17	112	4.8	1597	2	Q3U3D7_MOUSE	Q3u3d7 mus musculu
18	111.5	4.8	593	2	Q21VH2_RHOP2	Q21vh2 rhodospseudo
19	110.5	4.8	1384	2	Q3E1V7_CHLAU	Q3e1v7 chloroflexu
20	110.5	4.8	1390	2	Q8FX84_METMA	Q8fx84 methanosarc
21	110	4.7	519	2	Q51R80_TRAVE	Q51r80 trametres ve
22	109.5	4.7	1045	2	Q76037_HUMAN	Q76037 homo sapien
23	109.5	4.7	1475	2	Q5T9I7_HUMAN	Q5t9i7 homo sapien
24	109	4.7	519	1	LAC2_TRAVE	Q12718 trametres ve
25	109	4.7	519	1	LAC2_TRAVI	Q95046 trametres vi
26	109	4.7	519	2	Q50JG5_TRAVE	Q50jg5 trametres ve
27	108.5	4.7	783	2	Q5RMX8_CRYNE	Q5rmx8 cryptococcu
28	108.5	4.7	783	2	Q55X04_CRYNE	Q55x04 cryptococcu
29	108	4.7	519	2	Q96UK8_TRAVE	Q96uk8 trametres ve
30	108	4.7	720	2	Q32DV7_SHIDS	Q32dv7 shicella dy
31	108	4.7	725	2	Q5AJJ5_CANAL	Q5ajj5 candida alb
32	108	4.7	957	2	Q9UKN0_HUMAN	Q9ukn0 homo sapien
33	108	4.7	2281	2	Q5IT20_9CALI	Q5it20 sapovirus s
34	108	4.7	2287	2	Q1E9D6_COCIM	Q1e9d6 coccidioid
35	107.5	4.6	605	2	Q94K06_ARATH	Q94k06 arabidopsis
36	107.5	4.6	944	2	Q9UP82_HUMAN	Q9up82 homo sapien
37	107	4.6	1713	2	Q8TGE1_YEAST	Q8tge1 saccharomyc
38	107	4.6	2520	2	Q4MNM6_BACCE	Q4nm6 bacillus ce
39	106.5	4.6	1227	2	Q301T2_STRSU	Q301t2 streptococc
40	106	4.6	2280	2	Q6XDK9_9CALI	Q6xdk9 sapovirus m
41	105.5	4.5	463	2	Q5EBY5_9APHY	Q5eby5 lentinus ti
42	105.5	4.5	1829	2	Q1FED6_9CHLR	Q1fed6 roseiflexus
43	105.5	4.5	2520	2	Q637G8_BACGZ	Q637g8 bacillus ce
44	105	4.5	493	2	Q6ZNI4_HUMAN	Q6zni4 homo sapien
45	105	4.5	628	1	GIDA_TREDE	Q73phi treponema d

### ALIGNMENTS

RESULT 1  
Q96RK2\_HUMAN  
ID Q36RK2\_HUMAN PRELIMINARY; PRT; 6995 AA.  
AC Q96RK2;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2004, sequence version 2.  
DT 18-APR-2006, entry version 14.  
DE Mucin 16 (Fragment).  
GN Name=MUC16;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;

CC	Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RI	[1]
RN	NUCLEOTIDE SEQUENCE.
RP	MEDLINE=21347965; PubMed=11369781; DOI=10.1074/jbc.M103554200;
RX	Yin B.W., Lloyd K.O.;
NA	"Molecular cloning of the cal25 ovarian cancer antigen. identification
RT	as a new mucin, muc16.";
RT	J. Biol. Chem. 276:27371-27375(2001).
RL	[2]
RN	NUCLEOTIDE SEQUENCE.
RP	Lloyd K.O., Yin B.W.T.;
RA	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	EMBL; AF361486; AAK74120.3; -; mRNA.
DR	HSP; Q9DIH1; 11VZ.
DR	SMR; Q96RK2; 6809-6922.
DR	InterPro: IPR000194; ATPase_a_b_rl-bd.
DR	InterPro: IPR000082; SEA.
DR	Pfam: PF01390; SEA; 21.
DR	SMART; SM00200; SEA; 1.
DR	PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR	PROSITE; PS50024; SEA; 6.
FT	NON TER 1
SQ	SEQUENCE 6995 AA; 744966 MW; 80C797DBDF33A2B CRC64;

Query Match	99.8%	Score 2317	DB 2	Length 6995;	
Best Local Similarity	99.8%	Pred. No. 4.7e-165;			
Matches 438;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Db	6240	FTHRSSVSTTSPGCTPTVYLGA	SKTASIFG	PSAASHLLILFTLNFTITNLR	YEENWPG 6299
Qy	61	SKRNTTERRVLOGLLRPLKFN	TSVGPLYSG	RCRTLRLRPEKOG	ATGVDAICTHRPDPGP 120
Db	6300	SKRNTTERRVLOGLLRPLKFN	TSVGPLYSG	RCRTLRLRPEKOG	ATGVDAICTHRPDPGP 6359
Qy	121	GLDREQLYLELSQTHSIFEL	GPLGTYLDR	OSLYVNGFTHRSS	VPTTSTGWSSEPFNT 180
Db	6360	GLDREQLYLELSQTHSIFEL	GPLGTYLDR	OSLYVNGFTHRSS	VPTTSTGWSSEPFNT 6419
Qy	181	INNRLYMDWGPGSLKFNIT	DNYMKHLLS	PLFORSSLGARYTC	GRVIALRSVKNGAETR 240
Db	6420	INNRLYMDWGPGSLKFNIT	DNYMKHLLS	PLFORSSLGARYTC	GRVIALRSVKNGAETR 6479
Qy	241	VDLCTTYLQPLSGPLPIKQV	FHELSQOOTHG	ITLGPYSLDKDS	LYLINGINEPGPEPT 300
Db	6480	VDLCTTYLQPLSGPLPIKQV	FHELSQOOTHG	ITLGPYSLDKDS	LYLINGINEPGPEPT 6539
Qy	301	TKPATFTFPPUS	EATTFANGYHLK	TLTNFTINLQY	SPDMKGSATFNTSGVLOHLR 360
Db	6540	TKPATFTFPPUS	EATTFANGYHLK	TLTNFTINLQY	SPDMKGSATFNTSGVLOHLR 6599
Qy	361	PLFQKSSMGFFYLGCQIL	SILRPEXDG	AAATGVDTTCTY	HPDPVPGGLDIQQLYWELSQLTH 420
Db	6600	PLFQKSSMGFFYLGCQIL	SILRPEXDG	AAATGVDTTCTY	HPDPVPGGLDIQQLYWELSQLTH 6659

QY	421	GVTLGFWLDRDLSLFG	439
Db	6660	GVTLGFWLDRDLSLFG	6678
RESULT 2			
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ID	Q9H7S7_HUMAN	PRELIMINARY;	PRT: 1148 AA.
AC	Q9H7S7;		
DT	01-MAR-2001,	integrated into UniProtKB/TrEMBL.	
DT	01-MAR-2001,	sequence version 1.	
DT	18-APR-2006,	entry version 20.	
DE	CNA EJL14303 fis,	clone PLACE2000132.	
OS	Homo sapiens (human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;		
OC	Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NCBIREFSEQ: NC_000001.11		
RC	TISSUE=Placenta.		
RC	PubMed=14702039; DOI=10.1038/ng1285;		
RA	Oka T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,		
RA	Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,		
RA	Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,		
RA	Yanamoto J., Saito K., Isono Y., Shibano Y., Nakamura Y., Nagahari K.,		
RA	Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,		
RA	Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,		
RA	Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,		
RA	Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,		
RA	Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,		
RA	Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,		
RA	Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,		
RA	Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,		
RA	Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,		
RA	Matsushino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,		
RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,		
RA	Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,		
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,		
RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,		
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,		
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,		
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,		
RA	Kawabata A., Hixiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,		
RA	Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,		
RA	Matsuura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,		
RA	Toqashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,		
RA	Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,		
RA	Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,		
RA	Nakai K., Iada T., Nakamura Y., Ohara O., Isozaki T., Sugeno S.;		
RT	Complete sequencing and characterization of 21,243 full-length human		
RT	cDNAs."		
RL	Nat. Genet. 36:40-45(2004).		
CC			
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CC	Distributed under the Creative Commons Attribution-NoDerivs License		
CC			
DR	EMBL; AK024365; BAB14899.1; -; mRNA.		
DR	HSSP; Q9D1H1; 11V2.		
DR	SMR; Q9H7S7; 962-1075.		
DR	InterPro; IPR000082; SEA.		



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DR Pfam: PF01390; SEA; 8.
DR PROSITE: PS0024; SEA; 3.
SQ SEQUENCE 1148 AA; 127958 MW; 3861B0D5EFD8ABC CRC64;

Query Match          99.1%; Score 2301; DB 2; Length 1148;
Best Local Similarity 99.5%; Pred. No. 6.3e-163;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTHRSVSTSTGCTPTVYLGASKTPASIFGSPSAASHLLILFTLNFTITNLYEENMWPG 60
DB 1 FTHRSVSTSTGCTPTVYLGASKTPASIFGSPSAASHLLILFTLNFTITNLYEENMWPG 60
QY 61 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 120
DB 61 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 120
QY 453 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 512
DB 453 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 512
QY 121 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
DB 121 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
QY 513 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 572
DB 513 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 572
QY 181 INNLRYMADMGQPGSLKFNITDNVVKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 240
DB 181 INNLRYMADMGQPGSLKFNITDNVVKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 240
QY 573 INNLRYMADMGQPGSLKFNITDNVVKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 632
DB 573 INNLRYMADMGQPGSLKFNITDNVVKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 632
QY 241 VDLCTYLIQPLSGGPIPIKQVFHELSSQTHGITRLGPIYSLDKDSLYLNGYNEPGDEPPT 300
DB 241 VDLCTYLIQPLSGGPIPIKQVFHELSSQTHGITRLGPIYSLDKDSLYLNGYNEPGDEPPT 300
QY 693 TPKEATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 752
DB 693 TPKEATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 752
QY 361 PLFKSSKSGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 420
DB 361 PLFKSSKSGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 420
QY 421 GVTQLGFYVLDRLSLFING 439
DB 421 GVTQLGFYVLDRLSLFING 439
DB 813 GVTQLGFYVLDRLSLFING 831

RESULT 3
Q8WXI7_HUMAN PRELIMINARY; PRT; 22152 AA.
AC Q8WXI7;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 2.
DT 13-JUN-2006, entry version 18.
DE Ovarian cancer related tumor marker CA125.
GN Name=WUC16;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21646939; PubMed=11786729; DOI=10.1159/000050638;
RA O'Brien T.J., Beard J.B., Underwood L.J., Dennis R.A., Santin A.D.,
RA York L.;
RT "The CA 125 gene: an extracellular superstructure dominated by repeat
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sequences.";
RL Tumour Biol. 22:348-366(2001).
RP [2]
RN NUCLEOTIDE SEQUENCE.
RA O'Brien T.J., Underwood L.J., Beard J.B.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AF414442; AAL65133.2; -; mRNA.
DR SMR: Q8WXI7; 21966-22079.
DR Ensembl: ENSG00000181143; Homo sapiens.
DR HGNC: HGNC:15582; MUC16.
DR GO: GO:0019898; C:extrinsic to membrane; IDA.
DR GO: GO:0005515; F:protein binding; IPI.
DR GO: GO:0007155; P:cell adhesion; NAS.
DR InterPro: IPR000194; ATPase_a_b_n1-bd.
DR Pfam: PF01390; SEA; 56.
DR SMART: SM00200; SEA; 1.
DR PROSITE: PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR PROSITE: PS0024; SEA; 11.
SQ SEQUENCE 22152 AA; 2353428 MW; B3E7B0F19997A440 CRC64;

Query Match          99.1%; Score 2301; DB 2; Length 22152;
Best Local Similarity 99.5%; Pred. No. 3.7e-163;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTHRSVSTSTGCTPTVYLGASKTPASIFGSPSAASHLLILFTLNFTITNLYEENMWPG 60
DB 21397 FTHRSVSTSTGCTPTVYLGASKTPASIFGSPSAASHLLILFTLNFTITNLYEENMWPG 21456
QY 61 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 120
DB 21457 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 21516
QY 121 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
DB 21517 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 21576
QY 181 INNLRYMADMGQPGSLKFNITDNVVKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 240
DB 21577 INNLRYMADMGQPGSLKFNITDNVVKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 21636
QY 241 VDLCTYLIQPLSGGPIPIKQVFHELSSQTHGITRLGPIYSLDKDSLYLNGYNEPGDEPPT 300
DB 21637 VDLCTYLIQPLSGGPIPIKQVFHELSSQTHGITRLGPIYSLDKDSLYLNGYNEPGDEPPT 21696
QY 301 TPKEATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
DB 21697 TPKEATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 21756
QY 361 PLFKSSKSGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 420
DB 21757 PLFKSSKSGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 21816
QY 421 GVTQLGFYVLDRLSLFING 439
DB 21817 GVTQLGFYVLDRLSLFING 21835
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RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,  
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Varardo R., Wei C.L., Yagi K.,  
RA Yamaniishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
RA Grimmer S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
RA Wahlstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.,  
RA "The transcriptional landscape of the mammalian genome.";  
RT Science 309:1559-1563(2005).  
RN [31]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Whole body;  
RC PubMed=16141073; DOI=10.1126/science.1112009;  
RG RIKEN Genome Exploration Research Group, and Genome Science Group  
RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566(2005).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA NiKaido I., Osato N., Saito R., Suzuki H., Yamahara I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Clothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lennhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Sasaki D., Shibata K., Shinagawa A.,  
RA Birney E., Hayashizaki Y.,  
RA "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [15]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Whole body;  
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055000;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
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RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., De Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., King B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
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RA Hayashizaki Y.,  
RA "Functional annotation of a full-length mouse cDNA collection.";  
RT Nature 409:685-690(2001).  
RN [6]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Whole body;  
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multipillar sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [8]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Whole body;  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Soabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.,  
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RN NUCLEOTIDE SEQUENCE.  
RP STRUCTURE BY NMR OF 67-185.  
RX PubMed=14764598; DOI=10.1074/jbc.M309417200;  
RA Maeda T., Inoue M., Koshiba S., Yabuki T., Aoki M., Nunokawa E.,  
RA Seki E., Matsuda T., Motoda Y., Kobayashi A., Hiroyasu F.,

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RA Shirouzu M., Terada T., Hayami N., Ishizuka Y., Shinya N.,
RA Tatsuguchi A., Yoshida M., Hirota H., Matsuo Y., Tani K., Arakawa T.,
RA Carninci P., Kawai J., Hayashizaki Y., Kigawa T., Yokoyama S.;
RT "Solution structure of the SEA domain from the murine homologue of
RL ovarian cancer antigen CA125 (MUC16).";
RL J. Biol. Chem. 279:13174-13182(2004).
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CC -----
DR EMBL; AK003577; BAB22869.1; -; mRNA.
DR PDB; 1IVZ; NMR; A=67-185.
DR Ensembl; ENSMUSG00000032134; Mus musculus.
DR MGI; MGI:1920982; 1110008114Rik.
DR InterPro; IPR000082; SEA.
DR Pfam; PF01390; SEA; 1.
DR PROSITE; PS0024; SEA; 1.
KW Hypothetical protein.
SQ SEQUENCE 258 AA; 29426 MW; B64D9B63394D84E7 CRC64;

Query Match 9.3%; Score 217; DB 2; Length 258;
Best Local Similarity 35.3%; Pred. No. 5.2e-08;
Matches 49; Conservative 35; Mismatches 49; Indels 6; Gaps 4;

Qy 160 SSVPTTGTGVSEEPFTINTINRYMADMGPGSLKFNITDNVKKHLLSPLFRSSIG 219
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Db 61 AEIPTS---SSQENFLNTIPLPYSQIAQPTTYQTKRSTENALNQLFRNSSIK 117
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Qy 220 ARYTCGVIALRSV-KNGAETRVLLCTYLPGLPIKOVFHELSQOOTHGTRUGPY 278
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Db 118 SFSDQCVLAFRSVNNNTGVDSLCNF-SPLA-RRVDRVAIYEFLEFRTHTNGTOLLNF 175
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Qy 279 SLDKDSLYLINGNEPGDE 297
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Db 176 TLDRKSVFVDGYSQNRDD 194
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :

RESULT 6
Q8DKGO SYNEL PRELIMINARY; PRT: 729 AA.
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AC Q8DKGO;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DE 13-JUN-2006, entry version 20.
DE Two-component sensor histidine kinase.
GN OrderedLocustNames=t110899;
OC Synecococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32046;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834; DOI=10.1093/dnares/9.4.123;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RL Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
CC -----
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CC -----
DR EMBL; BA000039; BAC08451.1; -; Genomic_DNA.
DR GenomeReviews; BA000039.GR; t110899.
DR Biocyc; TEL0197221.T110899-MONOMER; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000155; F:two-component sensor activity; IEA.
DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .); IEA.
DR InterPro; IPR003594; ATP bd ATPase.
DR InterPro; IPR011006; CheY_like.
DR InterPro; IPR003018; GAF_like.
DR InterPro; IPR009082; His_kin_homodim.
DR InterPro; IPR004358; His_kin_like_C.
DR InterPro; IPR003661; His_kinA_N_.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR013516; PhvIo.chromo_BS.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; HiskA; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HiskA; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0046; PHYTOCHROME_2; 1.
KW Complete proteome; Kinase.
SQ SEQUENCE 729 AA; 82026 MW; 6E18ABA1666381B8 CRC64;

Query Match 5.1%; Score 117.5; DB 2; Length 729;
Best Local Similarity 22.3%; Pred. No. 7.5;
Matches 88; Conservative 43; Mismatches 119; Indels 145; Gaps 19;

Qy 117 PTGCLDREQLYLE-----LSQTHSITELGPYTLDRSLYNGFT----- 157
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Db 389 PLGLPTAKREYLEIIEHESGTHLELINSILDSEAEIGRSQLSAFSIRQLCADCLEV 448
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Qy 158 -----HRSSVPTTSTGVVSE---EPFTLNFTINNLRYMADMGQ----- 192
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Db 449 VKPQARRHQVNLRHQLMIPTRDRFWGDRYRIQIILINILLSNAIKFTPMGEVILRAWMK 508
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Qy 193 PGSLKENITD---NVMKHLLSPLFR-----SSLGARYTGCVRVIALRSVKNGAETRVDLL 244
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Db 509 EDELIFQVQDTGIGIPAHLASLLFKFQQLDSSFGRAYTG----- 548
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Qy 245 CTYLPQLSGGLPIKOVFHELSQOOTHGTRUGPYSLDKDSLYLING-----YNEPGDEP-P 299
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Db 549 -----AGLGLATKQWDLH---HG-----WIDVDSTEGKGSTFTVGLPALSIDL 591
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Qy 300 TTPKPTFTPLPLPS-----EAT-----TAKGYHLKTLTNFTIS 333
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Db 592 DPPKPKLD-VPLPLATTEVLVEPEGRIVLVSEDEATSLICSILTAGYQVIMLVDEGEVER 650
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
Qy 334 NQIYSYPMKSGKSGATNSTEGVLOHLRLPLFOK---SSMGPTFLCCQLISLRKDGGAATG 390
: : : : : I : I I I I I I I I : : : : : I : : : I : I I :
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Db 651 LLAUTPIAVLLAEPT--SYGVOELVDQORCTPEQLKIFILGSK-----GNYQG 699  
Qy 391 VOTTCYHPDPVGPGLDIQQLYWELSQLTHGVTOL 425  
Db 700 VD---RYIPLTHPESFLQ-----QVTGLTSL 724  
RESULT 7  
Q2FND5 METHJ PRELIMINARY; PRT; 865 AA.  
AC Q2FND5  
DT 21-MAR-2006, integrated into UniProtKB/TrEMBL.  
DT 11-JUL-2006, entry version 4.  
DE PKD.  
GN OrderedLocusNames=Mhun\_2522;  
OS Methanospirillum hungatei (strain JF-1 / DSM 864).  
OC Archaea; Euryarchaeota; Methanomicrobia; Methanomicrobiales;  
OC Methanospirillaceae; Methanospirillum.  
OX NCBI\_TaxID=323259;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).  
RG US DOE Joint Genome Institute;  
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,  
RA Hammon N., Israni S., Pitluck S., Brettin T., Bruce D., Han C.,  
RA Tapia R., Glinn P., Kiss H., Schmutz J., Larimer F., Land M.,  
RA Kyripides N., Ivanova N., McInerney M.J., Brockman F., Culley D.,  
RA Ferry J.G., Gunsalus R.P., Morrison M., Plugge C., Scholten J.,  
RA Stams A.J.M., Boone D.R., Richardson P.;  
RA "Complete sequence of Methanospirillum hungatei JG-1.";  
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL; CP000254; AB042222.1; --; Genomic DNA.  
DR GenomeReviews; CP000254.GR; Mhun\_2522.  
DR InterPro; IPR000601; PKD.  
DR Pfam; PF00801; PKD; 5.  
DR SMART; SM00089; PKD; 8.  
DR PROSITE; PS50093; PKD; 8.  
KW Complete proteome.  
SQ SEQUENCE 865 AA; 95487 MW; 9B41DEC0B9217191 CRC64;

Query Match 5.0%; Score 115.5; DB 2; Length 865;  
Best Local Similarity 20.7%; Pred. No. 13;  
Matches 74; Conservative 56; Mismatches 132; Indels 95; Gaps 18;  
Qy 24 KTPASIFGSAASHLLIFLTIN---FTTNURVEENWFGSRKNTERTVRLQGLRLPK 80  
Db 257 KSPVHCYEPGLYVSMYTIIDGAPYTIITKNRYLKYVPAGTDFATP--VEG----- 307  
Qy 81 NTSVGPL---YSCRLTLLRPEXGDE-----ATGVDAICTHRDPD\*GPGDLRSQLYLEL 131  
Db 308 ---IAPLCVAIS-----VINPTOSWEFNFGDNSTATSAQATHCYGTSN-----YF 350  
Qy 132 SQHTSIITEAGPYTLDRSSVPTTSTGTGVSEEPFTLNFTINLRVWADWG 191  
Db 351 PSITCYSCNNLCDTVEGKEPILV----HQPRILIAQGSALNEYKESTD-APEGLKYSWDG 405

Qy 192 Q-----PGSLKFNITDNVKKHLLSPLFORSSLGARYT--GCRVIALRSVKNGAETRVDL 243  
Db 406 DGTRAEGPAPSHRFDMEGT-----YRVSLVVTGTGCGNAIAVKELKMKPKGLDF 455  
Qy 244 LCTYLQPLSG-----PCLPTKQVPH-----ELSQOT---HGITRLGPGYSLDKDS 284  
Db 456 TAT---PLAGCAPHCVCQFNKSPSEIPLSRVMDFGDGETSEKNPFCRFPFGPYTVSUTD 512  
Qy 285 LYLINGYNEPGDEPPT---TPKPATTFPLPSEATTANGVYHLKTLTLTNFTISNLOYVS 338  
Db 513 TFPNGTQOEKVENYITAHAVKPSFTMFPHGDA-----PLTVKFTDFTVDYA 560  
RESULT 8  
Q16X85 AEDAE PRELIMINARY; PRT; 531 AA.  
AC Q16X85  
DT 25-JUL-2006, integrated into UniProtKB/TrEMBL.  
DT 25-JUL-2006, sequence version 1.  
DE Hypothetical protein.  
GN ORFNames=AaeI\_AAEI008949;  
OS Aedes aegypti (Yellowfever mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;  
OC Culicinae; Culicini; Aedes; Stegomyia.  
RX NCBI\_TaxID=7159;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RG STRAIN=Liverpool;  
RG The Broad Institute Genome Sequencing Platform;  
RA Loftus B.J., Nene V.M., Wortman J.R., Severson D.W., Collins F.,  
RA Galagan J., Devon K., Henn M.R., Jaffe D., Rounsley S., DeCaprio D.,  
RA Kodira C., Lander E., Crawford M., Hannick L.I., Bidwell S., Haas B.,  
RA Amedeo P., Orvis J., White O.R., Shumway M., Koo H., Zhao Y.,  
RA Holmes M., Miller J., Schatz M., Pop M., Salzberg S., Pal G.,  
RA Utterback T., Rogers Y.-H., Kravitz S., Butler J., Alvarez P.,  
RA Gnerre S., Grabherr M., Kleber M., Mauceli E., Brockman M., Young S.,  
RA LaButti K., Pushparaj V., Koehrsen M., Engels R., Montgomery P.,  
RA Pearson M., Howarth C., Zeng O., Yandava C., O'Leary S., Alvarado L.,  
RA Nusbaum C., Birren B., Fraser C.M.;  
RT "The Genome Sequence of Aedes aegypti (strain Liverpool).";  
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Liverpool;  
RA Loftus B.J., Nene V.M., Hannick L.I., Bidwell S., Haas B., Amedeo P.,  
RA Orvis J., Wortman J.R., White O.R., Salzberg S., Shumway M., Koo H.,  
RA Zhao Y., Holmes M., Miller J., Schatz M., Pop M., Pal G.,  
RA Utterback T., Rogers Y.-H., Kravitz S., Fraser C.M.;  
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL; CH477545; EAT39234.1; --; Genomic DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 531 AA; 56921 MW; F9BA04611ABF2350 CRC64;  
Query Match 5.0%; Score 115; DB 2; Length 531;  
Best Local Similarity 23.0%; Pred. No. 7.5;

Matches	91; Conservative	59; Mismatches	125; Indels	120; Gaps	24;
QY	7 VSTTSTPGTPTVYLGAASKTPASIFGSAASHLLILFTLNTLRYEENMMPGSRKFT	66			
RA	Beausoleil S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,				
DB	3 ITTSVKPESDVF-----ESATNELPLYSIDFSLVPKTPESNLT-SRVNT 48				
QY	67 TERVLQG--LLRPLFNKTSVGLYSGRLTLRLPEKDGATGVDAICTHRPDPTGPGDLR 124				
DB	49 NSAAAIIGDRSRMSIATNERPL--SCOTLEFNH-----ESYSCDSISEFTPN-----LAD 96				
QY	125 EQLYL-----ELSQLTHSITELGP-----YTL-----DRDSLIV--NGFT 157				
DB	97 QELYSSFSDFDSETSRYYSACHDLPFFHYKYPILSSRAUSYTSNDPERONLMPFNYS 156				
QY	158 HRSSVPTTSGVSWSEEPFTLNTLNNRYMDMGQSGSLKENITDNVM---KH-----L 208				
DB	157 YKML-YASTPLYSK-----SFDDLDYLDVOTPRNLENGSTATLENVKHSSPSPKS 208				
QY	209 LSPFLORS-SIGARYTGCRVIALRSVKNCAETRVLDLCTYLQPLSGPLIK-QVFEHLS 266				
DB	209 LSQTEARSGSHRPVT-----FSSPDN-----LTMIRVASDPLGPFRRSVTPTKD 253				
QY	267 QOTHGILTRGLYSLD--KDSLYLNGYNRGPDEPPTPK-----PATFLP 310				
DB	254 QPOSPT--DPTNDTQDTITFVSLTPTPPDEPFDLSALORDFOCLLDRMPFVSTELE 311				
QY	311 ---PL-----SEATTANGYHLKTLTLNFTSNL 335				
DB	312 KCPVVASASSDESATLTTF---PITTNLASSNL 343				
RESULT 9					
NU153 HUMAN					
ID	NU153 HUMAN	STANDARD;	PROT: 1475 AA.		
AC	P49790:				
DT	01-OCT-1996, integrated into UniProtKB/Swiss-Prot.				
DT	25-JUL-2006, entry version 44.				
DE	Nuclear pore complex protein Nup153 (Nucleoporin Nup153) (153 kDa				
DE	nucleoporin).				
GN	Name=NUP153;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;				
OC	Catarrhini; Hominiidae; Homo.				
OX	NCBI_TaxID=9606;				
ON	[1]				
RP	NUCLEOTIDE SEQUENCE [MRNA].				
RA	MEDLINE=94154002; PubMed=110839; DOI=10.1016/0167-4781(94)90040-X;				
RA	McKerrow I., Bastos R., Horton H., Burke B.;				
RT	"Sequence analysis of a cDNA encoding a human nuclear pore complex				
RT	protein, hnup153.";				
RL	Biochim. Biophys. Acta 1217:219-223(1994).				
RN	[2]				
RP	INTERACTION WITH XPO5.				
RX	MEDLINE=21640442; PubMed=1177942; DOI=10.1083/jcb.200110082;				
RA	Brownawell A.M., Macara I.G.;				
RT	"Exportin-5, a novel karyopherin, mediates nuclear export of double-				
RT	stranded RNA binding proteins.";				
RL	J. Cell Biol. 156:53-64(2002).				
RN	[3]				

RP	PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-529, AND MASS	
RP	SPECTROMETRY.	
RX	PubMed=15302935; DOI=10.1073/pnas.0404720101;	
RA	Beausoleil S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,	
RA	Li J., Cohn M.A., Cantley L.C., Gygi S.P.;	
RT	"Large-scale characterization of HeLa cell nuclear phosphoproteins.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).	
CC	-FUNCTION: Possible DNA-binding subunit of the nuclear pore complex	
CC	(NPC). The repeat-containing domain may be involved in anchoring	
CC	components of the pore complex to the pore membrane.	
CC	-SUBUNIT: Interacts with SENP2 and XPO5.	
CC	-SUBCELLULAR LOCATION: Nucleus; nuclear envelope; nuclear pore	
CC	complex. Located to the terminal ring structure of the	
CC	nucleoplasmic cage.	
CC	-DOMAIN: Contains F-X-F-G repeats.	
CC	-SIMILARITY: Contains 4 RanBP2-type zinc fingers.	
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CC	EMBL; Z25535; CAA80982.1; -; mRNA.	
DR	PIR; S42718; S42718.	
DR	Ensembl; ENSG00000124789; Homo sapiens.	
DR	HGNC; HGNC:8062; NUP153.	
DR	MIM; 603948; gene.	
DR	Reactome; P49790; -.	
DR	GO; GO:0005643; C:nuclear pore; TAS.	
DR	GO; GO:0005151; F:protein binding; IPI.	
DR	GO; GO:0005215; F:transporter activity; TAS.	
DR	InterPro; IPR001876; Znf_RanBP2.	
DR	Pfam; PF00641; zf-RanBP; 4.	
DR	SMART; SM00547; Znf_RBZ; 4.	
DR	PROSITE; PS01358; ZF_RANBP2_1; 4.	
DR	PROSITE; PS01099; ZF_RANBP2_2; 4.	
KW	DNA-binding; Metal-binding; Nuclear protein; Phosphorylation; Repeat;	
KW	Transport; Zinc; Zinc-finger.	
FT	CHAIN 1 1475 Nuclear pore complex protein Nup153.	
FT	/FtiD=PRO_0000204842.	
FT	ZN_FING 657 687 RanBP2-type 1.	
FT	ZN_FING 722 751 RanBP2-type 2.	
FT	ZN_FING 793 822 RanBP2-type 3.	
FT	ZN_FING 851 880 RanBP2-type 4.	
FT	ZN_COMPBIAS 4 14 Gly-rich.	
FT	COMPBIAS 443 447 Poly-Gly.	
FT	MOD_RES 529 529 Phosphoserine.	
FT	SEQUENCE 1475 AA; 153889 MW; 3CB415A6909DF80E CRC64;	
Query Match	4.98; Score 114.5; DB 1; Length 1475;	
Best Local Similarity	19.3%; Pred. No. 33;	
Matches	80; Conservative 53; Mismatches 149; Indels 133; Gaps 16;	
QY	17 TVYLGAASKTPASIFGSAASHLLILFTLNTLRYEENMMPGSRKFTTE 68	
DB	380 SVYFKPSLTPSG-----EERKTQRIIDNKSTGXEKNWTFQNR----E 419	
QY	69 RVLQGLRLFKNTSVGLYSGRLTLRLPEKDGATGVDAICTHRPDPTGPGDLREQY 128	
DB	420 QRESGFSYFNFS-----LPAANGLSSGVGG-----GGGKWRERH 454	
QY	129 LELSQLTHSITELGPLYTLDRDLSLVNGFTHRSVPT---TSTGVVSEEPFTLNTFT 183	



[illegible]

DT	04-APR-2006, entry version 16.
DE	RIKEN cDNA D930015E06.
DN	Name=D930015E06Rik;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Myrodonta; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RI	{1}
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6; TISSUE=Brain;
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA	Hopkins R.F., Jordan A., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA	Scherer A., Schein J.E., Jones S.J.M., Marra M.A.:
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RI	{2}
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6; TISSUE=Brain;
RG	NIH MGC Project;
RG	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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CC	-----
CC	EMBL; BC062940; AH62940.1; -; mRNA.
DR	UniGene; Mm.28838; -.
DR	Ensembl; ENSMUSG00000033767; Mus musculus.
DR	MGI; MGI:2443399; D930015E06Rik.
SQ	SEQUENCE 1386 AA; 152723 MW; 6FCE903EF167E372 CRC64;
Query Match	4.9%; Score 113.5; DB 2; Length 1386;
Best local Similarity	20.7%; Pred. No. 36;
Matches 113; Conservative	63; Mismatches 170; Indels 201; Gaps 2
Qy	59 PCSRKENTERVQGLRLPLFKN---TSVGPLYSGCRUTLLRPEKDEATGVDAIC---11
Db	300 PCGWNIISLKLAVGVLNVLTNTVTTNGAIFLQIPTSATRGK-SLGEVLAHCG 359
Qy	112 ----THRPDPTGPLDRQLYELISLTHSI-TELGYPTLDRDSLRYNG-----19
Db	359 MHYFNGSKSTENPWNERS---LSIDRSTWMDSELANKUYERWKKYSKGDACRRNVLMG 41
Qy	156 ----FTHRS---SVPTTS---TGVVSEEPFTYINLRYKA-----DKGPGSL-----19





RA	Schutz J., Larimer F., Land M., Kyripides N., Lykidis A., Moran M.A.,
RB	Belas R., Ye W., Buchan A., Gonzalez J.M., Schell M.A., Richardson P.,
RT	"Complete sequence of chromosome of <i>Jannaschia</i> sp. CCS1.",
RL	Submitted (FEB-2006) to the EMBL/GenBank/DBJ databases.
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CC	-----
CC	EMBL: CP000264; AB056490.1; -; Genomic_DNA.
DR	GenomeReviews: CP000264 GR; Jann 3573.
DR	GO: GO:0005727; C:extrachromosomal circular DNA; IEA.
DR	GO: GO:0001620; C:membrane; IEA.
DR	GO: GO:0005309; F:calcium ion binding; IEA.
DR	GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR	InterPro: IPR002126; Cadherin.
DR	InterPro: IPR001434; DUF11.
DR	InterPro: IPR004025; MIP.
DR	InterPro: IPR010221; VCBS.
DR	Pfam: PF01345; DUF11 2.
DR	TIGRFAMS: TIGR01451; B ant repeat; 18.
DR	TIGRFAMS: TIGR01965; VCBS Repeat: 1.
DR	PROSITE: PS00221; MIP; UNKNOWN_1.
KW	Complete proteome; Hypothetical protein; Signal.
FT	SIGNAL 1 31 potential.
FT	SEQUENCE 3486 AA; 3555115 MW; 7C764B012E95F3A2 CRC64;
SQ	

Query Match	4.9%	Score 113;	DB 2;	Length 3486;
Best Local Similarity	21.7%;	Pred. No. 1.4e+02;		
Matches 103;	Conservative	56;	Mismatches 200;	Indels 116; Gaps 21;
Qy	5	SSVSTTSTPGTPPV-----YLGASKTASTASFGP--SAASHLLI-----LFTLFTFTNL	51	
Db	1045	TSGTTTSPVETVPVSGGTPALAKSKLLSITDPVGTASGLQFNEVGVDLITFTTFQVTN-	1103	
Qy	52	RYEENWGSRKNTTTERVLOGLLRP----LFWNTSVGLPYSGCRUTLLRPEKDGATGV	107	
Db	1104	-----NGTRKSVREVTVDVAMLTNPNTCTFTPGGPDF-----APGE	1141	
Qy	108	DAICTHRDPTGFLDRQLYLELSOLSTHSTLGTLPYLLDRDSLXYNGCFTHRSSVPTTST	167	
Db	1142	TVNCTQGVTVLADLDEE-----EWNVAFASVEEGAPPNNSTSVY--NSPSAQATVPALAA	1196	
Qy	166	GWVS-----EEP-----FTLNTFINILRYWADGPGPSLKNFITDNWKKHLSP	211	
Db	1197	PAUTVAKVDTAGDPASAGVDVLTITATNSGNTQLSDVS-----LSDP	1240	
Qy	212	LFORSSIGARVTCGRVIALRSVKNGATRVDRLLCTYLQPLSGPLP;KQVFHELSOOTHG	271	
Db	1241	LI--PSLUCTVGGVPANVTIAPGGV---LJCT-----GDYTVQANFDQMLSWT	1287	
Qy	272	ITRLGYPYSLDKDSLYLYNGINEPGDPPTPKPATFTLPLPEASEATTAMGYHLKTLTINT	331	
Db	1288	ATATG--LDPDGAQVSG--NRGDMHPLATPQPEMLIKTITAGTPTPAYTAANDAVSPT	1342	
Qy	332	ISNLOYSPDMKGSATENS--TEGVLOHLRLPLFKQSSMGPFYLG-----COLLSLRPE	383	
Db	1343	IE-----VRNVTGNVTLNSVAVDSIVVG-----TTCTVGLAPGASONSCRVTYTVLQ	1390	
Qy	384	KDGAATGVDTCTYHPDPVPGFLDIQILYWELSQLTHGVTLQFYVLDRLSLFIN	438	
Db	1391	SDWDAGQIDINWATGVATPI--PSSGAGQITRTGVLTITQGERPLPSISLEKADLAN	1444	

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RESULT 15
Q6WVDA_NEUCR PRELIMINARY; PRT; 1625 AA.
AC Q6WVDA;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Related to glucan 1, 4-alpha-glucosidase.
GN Name=B13D15.100;
GS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA German Neurospora genome project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BX842630; CAE76365.1; -: Genomic DNA.
SQ SEQUENCE 1625 AA; 156729 MW; 8FF65C0B88072B46 CRC64;

Query Match 4.8%; Score 112.5; DB 2; Length 1625;
Best local similarity 21.5%; Pred. No. 54;
Matches 101; Conservative 50; Mismatches 169; Indels 149; Gaps 233

Qy 5 SSVSTTSTGCTFVY---LGAKTPASIFGPSAASHLLILTLINFTITNLRYEENMWP 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 NSSSTSPRESSSGYSFSAUSSGSGTISGVTSASP-----TLNSTTTTLAFSTSG 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 61 -----SRKFNTERVQLLRLEKFNKTSVGLYSGLRLLRPEKDG-ATGVDA 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 227 TTSGYSSQSSSTENTI-----ALLDTTSA-----MSTSPNSASSETNPTSG 269

Qy 110 ICHRPDPGPGDLREQLYLEISQLTHISITELGPTLDRSLYVNGFTHRSVP----T 164
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 270 GTTSPSP-----SPVIVSVISVGP-----ESSSFKSPNETATIPPSTESS 311
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 165 TSTGVSEPFPTLNTLNRLRYMADMGQSGLKFNITDNVMKHLSP----- 212
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 312 STSLVASEFPF--FT-----NSSSPQT--SFPSGSGLTGVTTPPAKSSSSASGSG 360

Qy 213 ---FORSILGARYTCRVIALRSVKNGAETVDL-----LCTYLQPLSGPLPIKQ 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 361 GLPNSSSSIGSISAPFISASITLPSGSPPFPLTANSSSSPGLSCTLPPPSGTASV-- 418
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 261 VFHLSQOOTHGITRLGYSLDKDSLYL-NGYNEPCDEPPT----TKPATFTFLPSEA 315
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 419 -----TTSUSSSTFTSNSSSLPTGVSDGTTLPTSGSNLTSPAGTFTPPVSGS 467
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 316 TTAKGYHLKTLTNFTINLQYSPDMGKSGATFNSTEGVLIQHLRLPFOKSSNG---PF 372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 468 ILPSG---SSSAPFVTNLSAPLTGPTGSSSTTGSVTS-----QESSLSVPIPIIS 513  
Oy 373 LGCQLISLRPEKDGATG-----VDTTCTYHPD-----PVGPG 405  
Db 514 NSSEII---PSSTGAGLGSGSSMLPASSTIPVSSTYNLSSSSTVPITGTG 559

Search completed: June 7, 2007, 17:51:41  
Job time : 375 secs

SCORE 2.0 BuildDate: 12/05/2005
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# SCORE Search Results Details for Application 10687035 and Search Result 20070607\_154750\_us-10-687-035-1\_copy\_14\_452.rapbn.

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OM protein - protein search, using sw model  
Run on: June 7, 2007, 17:57:54 ; Search time 313 Seconds  
(without alignments)  
478.070 Million cell updates/sec  
Title: US-10-687-035-1\_COPY\_14\_452  
Perfect score: 2321  
Sequence: 1 FTHRSSVSTTPTGCTPTVYL.....HGVTQLGFVLDKDSLEIFNG 439

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1387086 seqs, 340856542 residues  
Total number of hits satisfying chosen parameters: 1387086  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:\*  
1: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
2: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
3: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
4: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*  
6: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*  
7: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /EMC\_Celeerra\_SID33/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2317	99.8	811	7	US-11-066-316A-961	Sequence 961, App
2	2317	99.8	811	7	US-11-066-316A-965	Sequence 965, App
3	2317	99.8	1890	7	US-11-582-861-6592	Sequence 6592, Ap
4	2317	99.8	13888	7	US-11-066-316A-963	Sequence 963, App
5	2311	99.6	1890	7	US-11-443-428A-775223	Sequence 775223,
6	2301	99.1	1148	6	US-10-475-117-48	Sequence 48, Appl
7	2301	99.1	1148	6	US-10-917-503-18865	Sequence 18865, A
8	2301	99.1	1148	7	US-11-105-233-195	Sequence 195, App
9	2301	99.1	1148	7	US-11-226-554-129	Sequence 129, App
10	2301	99.1	1148	7	US-11-248-718-129	Sequence 129, App
11	2301	99.1	1148	7	US-11-538-552-129	Sequence 129, App
12	2301	99.1	2248	6	US-10-475-117-50	Sequence 50, Appl
13	2301	99.1	9799	6	US-10-475-117-146	Sequence 146, App
14	2301	99.1	11721	6	US-10-475-117-162	Sequence 162, App
15	2301	99.1	22152	6	US-10-544-944-1	Sequence 1, Appli
16	2301	99.1	22152	6	US-10-475-117-315	Sequence 315, App
17	2301	99.1	22152	7	US-11-582-861-6593	Sequence 6593, Ap
18	2205.5	95.0	1307	6	US-10-777-288A-3696	Sequence 3696, Ap
19	2185	94.1	1647	6	US-10-777-288A-3700	Sequence 3700, Ap
20	2005.5	86.4	1832	7	US-11-443-428A-775224	Sequence 775224,
21	1512	65.1	867	6	US-10-777-288A-3863	Sequence 3863, Ap
22	1384.5	59.7	909	7	US-10-475-117-69	Sequence 69, Appl
23	1383.5	59.6	909	7	US-11-443-428A-775226	Sequence 775226,
24	1365.5	58.8	1366	6	US-10-475-117-47	Sequence 47, Appl
25	1348.5	58.1	780	6	US-10-475-117-159	Sequence 159, App
26	1348.5	58.1	780	6	US-10-475-117-158	Sequence 158, App
27	1322	57.0	594	6	US-10-475-117-71	Sequence 71, Appl
28	1317	56.7	594	6	US-10-475-117-71	Sequence 960, App
29	1314.5	56.6	12704	7	US-11-066-316A-960	Sequence 964, App
30	1314.5	56.6	12756	7	US-11-066-316A-964	Sequence 959, App
31	1314.5	56.6	12759	7	US-11-066-316A-959	Sequence 959, App
32	1303	56.1	597	6	US-10-475-117-78	Sequence 78, Appl
33	1284.5	55.3	525	6	US-10-475-117-70	Sequence 80, Appl
34	1250.5	53.9	479	6	US-10-475-117-80	Sequence 161, App
35	1242.5	53.5	468	6	US-10-475-117-161	Sequence 161, App
36	1214	52.3	12622	7	US-11-066-316A-962	Sequence 962, App
37	1181.5	50.9	443	6	US-10-475-117-42	Sequence 42, Appl
38	1159	49.9	439	6	US-10-475-117-39	Sequence 39, Appl
39	1112	47.9	420	6	US-10-475-117-38	Sequence 38, Appl
40	1112	47.9	420	6	US-10-475-117-79	Sequence 79, Appl
41	1110	47.8	438	6	US-10-475-117-37	Sequence 37, Appl
42	1080	46.5	424	6	US-10-475-117-40	Sequence 40, Appl
43	1080	46.5	424	6	US-10-475-117-72	Sequence 72, Appl
44	1076	46.4	442	6	US-10-475-117-44	Sequence 44, Appl
45	1066	45.9	386	6	US-10-475-117-36	Sequence 36, Appl

## ALIGNMENTS

RESULT 1  
US-11-066-316A-961  
; Sequence 961, Application US/11066316A  
; Publication No. US20070059710A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, May

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STROKE, METHODS OF  
; FILE REFERENCE: CL001585  
; CURRENT APPLICATION NUMBER: US/11/066, 316A  
; CURRENT FILING DATE: 2005-02-25  
; NUMBER OF SEQ ID NOS: 55503  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 961  
; LENGTH: 811  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-066-316A-961

Query Match 99.8%; Score 2317; DB 7; Length 811;  
Best Local Similarity 99.8%; Pred. No. 3e-179;  
Matches 438; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FTHRSSVSTTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60  
Db 56 FTHRSSVSTTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 115  
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDPGTP 120  
Db 116 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDPGTP 175  
Qy 121 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
Db 176 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 235  
Qy 181 INNLRYADMQPGSLKENITDNVWQHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 240  
Db 236 INNLRYADMQPGSLKENITDNVWQHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 295  
Qy 241 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 300  
Db 296 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 355  
Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPODMKGSATFNSTEGVLOHLRL 360  
Db 356 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPODMKGSATFNSTEGVLOHLRL 415  
Qy 361 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVPGGLDIOQLYWELSQLTH 420  
Db 416 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVPGGLDIOQLYWELSQLTH 475  
Qy 421 GVTQLGFYVLDKDSLFING 439  
Db 476 GVTQLGFYVLDKDSLFING 494

RESULT 2  
US-11-066-316A-965  
; Sequence 965, Application US/11066316A  
; Publication No. US20070059710A1  
; GENERAL INFORMATION:  
; APPLICANT: Luke, May  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STROKE, METHODS OF  
; FILE REFERENCE: CL001585  
; CURRENT APPLICATION NUMBER: US/11/066, 316A  
; CURRENT FILING DATE: 2005-02-25

; NUMBER OF SEQ ID NOS: 55503  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 965  
; LENGTH: 811  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-066-316A-965

Query Match 99.8%; Score 2317; DB 7; Length 811;  
Best Local Similarity 99.8%; Pred. No. 3e-179;  
Matches 438; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FTHRSSVSTTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60  
Db 56 FTHRSSVSTTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 115  
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDPGTP 120  
Db 116 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDPGTP 175  
Qy 121 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
Db 176 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 235  
Qy 181 INNLRYADMQPGSLKENITDNVWQHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 240  
Db 236 INNLRYADMQPGSLKENITDNVWQHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 295  
Qy 241 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 300  
Db 296 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 355  
Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPODMKGSATFNSTEGVLOHLRL 360  
Db 356 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPODMKGSATFNSTEGVLOHLRL 415  
Qy 361 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVPGGLDIOQLYWELSQLTH 420  
Db 416 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVPGGLDIOQLYWELSQLTH 475  
Qy 421 GVTQLGFYVLDKDSLFING 439  
Db 476 GVTQLGFYVLDKDSLFING 494

RESULT 3  
US-11-582-861-6592  
; Sequence 6592, Application US/11582861  
; Publication No. US20070099251A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Hui  
; APPLICANT: Aebersold, Rudolf H.  
; TITLE OF INVENTION: TISSUE- AND SERUM-DERIVED GLYCOPROTEINS  
; TITLE OF INVENTION: AND METHODS OF THEIR USE  
; FILE REFERENCE: 460092.404  
; CURRENT APPLICATION NUMBER: US/11/582,861  
; CURRENT FILING DATE: 2006-10-17  
; PRIOR APPLICATION NUMBER: US 60/728,044  
; PRIOR FILING DATE: 2005-10-17  
; NUMBER OF SEQ ID NOS: 14918  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 6592
; LENGTH: 1890
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-582-861-6592

Query Match          99.8%; Score 2317; DB 7; Length 1890;
Best Local Similarity 99.8%; Pred. No. 8.9e-179;
Matches 438; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||
Db 1135 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 1194

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLRPEKDEATGVDAICTHRPDPTGP 120
    |||
Db 1195 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLRPEKDEATGVDAICTHRPDPTGP 1254

Qy 121 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||
Db 1255 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 1314

Qy 181 INNLRYMADMQPGSLKENITDNVMKHLSPLFQSSGLGARYTGCVRVIALRSVKNGAETR 240
    |||
Db 1315 INNLRYMADMQPGSLKENITDNVMKHLSPLFQSSGLGARYTGCVRVIALRSVKNGAETR 1374

Qy 241 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGTRGLPGYSLDKDSLYLNGYNPEGDPDEPT 300
    |||
Db 1375 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGTRGLPGYSLDKDSLYLNGYNPEGDPDEPT 1434

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKGSATFNSTEGVLQHLR 360
    |||
Db 1435 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKGSATFNSTEGVLQHLR 1494

Qy 361 PLFKSSMGPFYLCQLISLRPEKDGATGVTCTTYHPDPVPGGLDIQQLYWELSQLTH 420
    |||
Db 1495 PLFKSSMGPFYLCQLISLRPEKDGATGVTCTTYHPDPVPGGLDIQQLYWELSQLTH 1554

Qy 421 GVTOLGFYVLDROSLFING 439
    |||
Db 1555 GVTOLGFYVLDROSLFING 1573

RESULT 4
US-11-066-316A-963
; Sequence 963, Application US/11066316A
; Publication No. US20070059710A1
; GENERAL INFORMATION:
; APPLICANT: Luke, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STROKE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001585
; CURRENT APPLICATION NUMBER: US/11/066.316A
; CURRENT FILING DATE: 2005-02-25
; NUMBER OF SEQ ID NOS: 55503
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 963
; LENGTH: 13888
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-066-316A-963
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Query Match          99.8%; Score 2317; DB 7; Length 13888;
Best Local Similarity 99.8%; Pred. No. 1.2e-177;
Matches 438; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
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Db 13133 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 13192

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLRPEKDEATGVDAICTHRPDPTGP 120
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Db 13193 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLRPEKDEATGVDAICTHRPDPTGP 13252

Qy 121 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||
Db 13253 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 13312

Qy 181 INNLRYMADMQPGSLKENITDNVMKHLSPLFQSSGLGARYTGCVRVIALRSVKNGAETR 240
    |||
Db 13313 INNLRYMADMQPGSLKENITDNVMKHLSPLFQSSGLGARYTGCVRVIALRSVKNGAETR 13372

Qy 241 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGTRGLPGYSLDKDSLYLNGYNPEGDPDEPT 300
    |||
Db 13373 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGTRGLPGYSLDKDSLYLNGYNPEGDPDEPT 13432

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKGSATFNSTEGVLQHLR 360
    |||
Db 13433 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKGSATFNSTEGVLQHLR 13492

Qy 361 PLFKSSMGPFYLCQLISLRPEKDGATGVTCTTYHPDPVPGGLDIQQLYWELSQLTH 420
    |||
Db 13493 PLFKSSMGPFYLCQLISLRPEKDGATGVTCTTYHPDPVPGGLDIQQLYWELSQLTH 13552

Qy 421 GVTOLGFYVLDROSLFING 439
    |||
Db 13553 GVTOLGFYVLDROSLFING 13571

RESULT 5
US-11-443-428A-775223
; Sequence 775223, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Wintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCE
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 775223
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; LENGTH: 1890
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-775223

Query Match          99.6%; Score 2311; DB 7; Length 1890;
Best Local Similarity 99.8%; Pred. No. 2.7e-178;
Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||
Db 1135 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 1194

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDALCTHRPDPGTP 120
    |||||||
Db 1195 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDALCTHRPDPGTP 1254

Qy 121 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 180
    |||||||
Db 1255 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 1314

Qy 181 INNLRYADMGMGPGSLKFNITDNWVKHLLSPFORSSLGARYTGCRIALRSVKNGAETR 240
    |||||||
Db 1315 INNLRYADMGMGPGSLKFNITDNWVKHLLSPFORSSLGARYTGCRIALRSVKNGAETR 1374

Qy 241 VDLCTYLPQLSGPLPIKQVFHELSQLQTHGITRLGPLYSLDKDSLXYNGYNEPGDEPPT 300
    |||||||
Db 1375 VDLCTYLPQLSGPLPIKQVFHELSQLQTHGITRLGPLYSLDKDSLXYNGYNEPGDEPPT 1434

Qy 301 TPKPATTELPPLSEATTANGYHLKTLTINFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
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Db 1435 TPKPATTELPPLSEATTANGYHLKTLTINFTISNLQYSPDMGKGSATFNSTEGVLQHLR 1494

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 420
    |||||||
Db 1495 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 1554

Qy 421 GVTOLGFYVLDRLDSLFG 439
    |||||||
Db 1555 GVTOLGFYVLDRLDSLFG 1573

RESULT 6
US-10-475-117-48
; Sequence 48, Application US/10475117
; Publication No. US20070015907A1
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Arkansas
; APPLICANT: O'Brien, Timothy
; APPLICANT: Beard, John
; APPLICANT: Underwood, Lowell
; TITLE OF INVENTION: CA125 Gene and its Use for Diagnostic and Therapeutic
; TITLE OF INVENTION: Interventions
; FILE REFERENCE: 022438.43867
; CURRENT APPLICATION NUMBER: US/10/475.117
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/US02/11734
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/284,175
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/299,380
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; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 09/965,738
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/427,045
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/345,180
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 48
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-475-117-48

Query Match          99.1%; Score 2301; DB 6; Length 1148;
Best Local Similarity 99.5%; Pred. No. 9.3e-178;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||
Db 393 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 452

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDALCTHRPDPGTP 120
    |||||||
Db 453 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDALCTHRPDPGTP 512

Qy 121 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSGVSEEPFTLNFT 180
    |||||||
Db 513 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSGVSEEPFTLNFT 572

Qy 181 INNLRYADMGMGPGSLKFNITDNWVKHLLSPFORSSLGARYTGCRIALRSVKNGAETR 240
    |||||||
Db 573 INNLRYADMGMGPGSLKFNITDNWVKHLLSPFORSSLGARYTGCRIALRSVKNGAETR 632

Qy 241 VDLCTYLPQLSGPLPIKQVFHELSQLQTHGITRLGPLYSLDKDSLXYNGYNEPGDEPPT 300
    |||||||
Db 633 VDLCTYLPQLSGPLPIKQVFHELSQLQTHGITRLGPLYSLDKDSLXYNGYNEPGDEPPT 692

Qy 301 TPKPATTELPPLSEATTANGYHLKTLTINFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
    |||||||
Db 693 TPKPATTELPPLSEATTANGYHLKTLTINFTISNLQYSPDMGKGSATFNSTEGVLQHLR 752

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 420
    |||||||
Db 753 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 812

Qy 421 GVTOLGFYVLDRLDSLFG 439
    |||||||
Db 813 GVTOLGFYVLDRLDSLFG 831

RESULT 7
US-10-917-503-18865
; Sequence 18865, Application US/10917503
; Publication No. US20070105122A1
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
```

APPLICANT: SAITO, KAORU  
APPLICANT: YAMAMOTO, JUNICHI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: NAKAMATSU, AI  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: OTSUKI, TETSUJI  
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE  
FILE REFERENCE: 084335/0123  
CURRENT APPLICATION NUMBER: US/10/917,503  
CURRENT FILING DATE: 2004-08-13  
PRIOR APPLICATION NUMBER: US/09/629,469  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: JP 1999-248036  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: JP 1999-300253  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: JP 2000-118776  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: JP 2000-183767  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: JP 2000-241899  
PRIOR FILING DATE: 2000-06-09  
PRIOR APPLICATION NUMBER: 60/159,590  
PRIOR FILING DATE: 1999-10-18  
PRIOR APPLICATION NUMBER: 60/183,322  
PRIOR FILING DATE: 2000-02-17  
NUMBER OF SEQ ID NOS: 19025  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 18865  
LENGTH: 1148  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-917-503-18865

Query Match 99.1%; Score 2301; DB 6; Length 1148;  
Best Local Similarity 99.5%; Pred. No. 9.3e-178;  
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSPGTPVYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENWMPG 60  
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Db 393 FTHRSSVSTTSPGTPVYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENWMPG 452

Qy 61 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRITLLRPEKDGATGDAICTHRPDPTGP 120  
|||||  
Db 453 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGSRITLLRPEKDGATGDAICTHRPDPTGP 512

Qy 121 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
|||||  
Db 513 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 572

Qy 181 INNLRYWADMGQPGSLKFNITDNVVKHLLSPLFORSSILGARYTCGRVIALRSVKNGAETR 240  
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Db 573 INNLRYWADMGQPGSLKFNITDNVVKHLLSPLFORSSILGARYTCGRVIALRSVKNGAETR 632

Qy 241 VOLLCITYLQPLSGPLPIKQVFHELSSQOHTGIFRLGPLYSLDKDSLYNGYNEPGDPPT 300  
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Db 633 VOLLCITYLQPLSGPLPIKQVFHELSSQOHTGIFRLGPLYSLDKDSLYNGYNEPGDPPT 692

Qy 301 TKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360  
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Db 693 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 752

Qy 361 PLFOKSSNGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQOLYWELSOLTH 420  
|||||  
Db 753 PLFOKSSNGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQOLYWELSOLTH 812

Qy 421 GVTQLGFVYLDRLDSLFING 439  
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Db 813 GVTQLGFVYLDRLDSLFING 831

RESULT 8  
US-11-105-233-195  
Sequence 195, Application US/11105233  
Publication No. US20060134653A1  
GENERAL INFORMATION:  
APPLICANT: Thiagalingam et al  
TITLE OF INVENTION: Differential Expression of Genes in MSI  
FILE REFERENCE: 1657/2001  
CURRENT APPLICATION NUMBER: US/11/105,233  
CURRENT FILING DATE: 2005-04-13  
NUMBER OF SEQ ID NOS: 202  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 195  
LENGTH: 1148  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-105-233-195

Query Match 99.1%; Score 2301; DB 7; Length 1148;  
Best Local Similarity 99.5%; Pred. No. 9.3e-178;  
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSPGTPVYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENWMPG 60  
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Db 393 FTHRSSVSTTSPGTPVYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENWMPG 452

Qy 61 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRITLLRPEKDGATGDAICTHRPDPTGP 120  
|||||  
Db 453 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGSRITLLRPEKDGATGDAICTHRPDPTGP 512

Qy 121 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
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Db 513 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 572

Qy 181 INNLRYWADMGQPGSLKFNITDNVVKHLLSPLFORSSILGARYTCGRVIALRSVKNGAETR 240  
|||||  
Db 573 INNLRYWADMGQPGSLKFNITDNVVKHLLSPLFORSSILGARYTCGRVIALRSVKNGAETR 632

Qy 241 VOLLCITYLQPLSGPLPIKQVFHELSSQOHTGIFRLGPLYSLDKDSLYNGYNEPGDPPT 300  
|||||  
Db 633 VOLLCITYLQPLSGPLPIKQVFHELSSQOHTGIFRLGPLYSLDKDSLYNGYNEPGDPPT 692

Qy 301 TKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360  
|||||  
Db 753 PLFOKSSNGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQOLYWELSOLTH 812



QY	421	GVTOLGFYVLDROSLFNG 439 
Db	813	GVTOLGFYVLDROSLFNG 831
RESULT 9		
US-11-226-554-129		
; Sequence 129, Application US/11226554		
; Publication No. US2006014737A1		
; GENERAL INFORMATION:		
; APPLICANT: Cairns,Belinda		
; APPLICANT: Chen,Ruihuan		
; APPLICANT: Frantz,Gretchen		
; APPLICANT: Hillan,Kenneth J.		
; APPLICANT: Koepfen,Hartmut		
; APPLICANT: Phillips,Heidi S.		
; APPLICANT: Polakis,Paul		
; APPLICANT: Spencer,Susan D.		
; APPLICANT: Smith,Victoria		
; APPLICANT: Williams, P. Mickey		
; APPLICANT: Wu,Thomas D.		
; APPLICANT: Zhang,Zemin		
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and		
; FILE OF INVENTION: Treatment of Tumor		
; FILE REFERENCE: F500IR1C1		
; CURRENT APPLICATION NUMBER: US/11/226,554		
; CURRENT FILING DATE: 2005-09-13		
; PRIOR APPLICATION NUMBER: US 10/177,488		
; PRIOR FILING DATE: 2002-06-19		
; PRIOR APPLICATION NUMBER: US 60/366,969		
; PRIOR FILING DATE: 2002-03-20		
; NUMBER OF SEQ ID NOS: 154		
; SEQ ID NO 129		
; LENGTH: 1148		
; TYPE: PRt		
; ORGANISM: Homo sapiens		
US-11-226-554-129		
Query Match 99.1%; Score 2301; DB 7; Length 1148;		
Best Local Similarity 99.5%; Pred. No. 9.3e-178;		
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	1	FTHRSSVSTTGTCTGYVLGASKTPTASIFGPSAAASHLLILFTITNLRYEENWPG 60 
Db	393	FTHRSSVSTTGTCTGYVLGASKTPTASIFGPSAAASHLLILFTITNLRYEENWPG 452 
QY	61	SRKENTERVLOGLLRLPFRKNTSVGLPSYSGCRUTLRLPEKDKGEATGVDAICTHRPDPTGP 120 
Db	453	SRKENTERVLOGLLRLPFRKNTSVGLPSYSGSRULTLLRPEKDKGEATGVDAICTHRPDPTGP 512 
QY	121	GDREQLYLELSQLTHTISILGPTYTLDRDSLYNGTHRSSVPPTTSTGWVSEEPFTLNPT 180 
Db	513	GDREQLYLELSQLTHTISILGPTYTLDRDSLYNGTHRSSVPPTTSTGWVSEEPFTLNPT 572 
QY	181	INNLRYMADMQPGSKLKFNITDNVMKHLLSPLFORSSLGARYTCGRVIALRSVKNGAEATR 240 
Db	573	INNLRYMADMQPGSKLKFNITDNVMKHLLSPLFORSSLGARYTCGRVIALRSVKNGAEATR 632 
QY	241	VOLLCTTYLQPLSGPGLPKQVFHELHESQQOHTGTRLAGPYSLDKDSLZYNGNEPGDPDEPT 300 

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-248-718-129

Query Match      99.1%; Score 2301; DB 7; Length 1148;
Best Local Similarity 99.5%; Pred. No. 9.3e-178;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
        |||||||
Db      393 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 452

QY      61  SRKENTTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
        |||||||
Db      453 SRKENTTTERVLOGLLRPLFKNTSVGPLYSGSRLLTLRPEKDGATGVDAICTHRPDPTGP 512

QY      121 GLDREQLYLELSQLTSHITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
        |||||||
Db      513 GLDREQLYLELSQLTSHITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 572

QY      181 INNLRYADMGMGPGSLKFNITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR 240
        |||||||
Db      573 INNLRYADMGMGPGSLKFNITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR 632

QY      241 VDLCTYLIQPLSGPLPIKQVFHELSSQOOTHGITRLGYPYSLDKDSLYLNGYNFPGPDEPPT 300
        |||||||
Db      633 VDLCTYLIQPLSGPLPIKQVFHELSSQOOTHGITRLGYPYSLDKDSLYLNGYNFPGPDEPPT 692

QY      301 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 360
        |||||||
Db      693 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 752

QY      361 PLFOKSSMGPGYLGCOLISLRPEKDGAAATGVDTCTTYHPDPVPGCLDIQOLYWELSQLTH 420
        |||||||
Db      753 PLFOKSSMGPGYLGCOLISLRPEKDGAAATGVDTCTTYHPDPVPGCLDIQOLYWELSQLTH 812

QY      421 GVTOLGFYVLDRLDSLEFNG 439
        |||||||
Db      813 GVTOLGFYVLDRLDSLEFNG 831

RESULT 11
US-11-538-552-129
; Sequence 129, Application US/11538552
; Publication No. US20070048326A1
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koepfen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1 US
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; CURRENT APPLICATION NUMBER: US/11/538,552
; CURRENT FILING DATE: 2006-10-04
; PRIOR APPLICATION NUMBER: US/11/248,718
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/300,880
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/304,813
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/312,312
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 60/314,280
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/339,227
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 129
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-538-552-129

Query Match      99.1%; Score 2301; DB 7; Length 1148;
Best Local Similarity 99.5%; Pred. No. 9.3e-178;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
        |||||||
Db      393 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 452

QY      61  SRKENTTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
        |||||||
Db      453 SRKENTTTERVLOGLLRPLFKNTSVGPLYSGSRLLTLRPEKDGATGVDAICTHRPDPTGP 512

QY      121 GLDREQLYLELSQLTSHITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
        |||||||
Db      513 GLDREQLYLELSQLTSHITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 572

QY      181 INNLRYADMGMGPGSLKFNITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR 240
        |||||||
Db      573 INNLRYADMGMGPGSLKFNITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR 632

QY      241 VDLCTYLIQPLSGPLPIKQVFHELSSQOOTHGITRLGYPYSLDKDSLYLNGYNFPGPDEPPT 300
        |||||||
Db      633 VDLCTYLIQPLSGPLPIKQVFHELSSQOOTHGITRLGYPYSLDKDSLYLNGYNFPGPDEPPT 692

QY      301 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 360
        |||||||
Db      693 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 752

QY      361 PLFOKSSMGPGYLGCOLISLRPEKDGAAATGVDTCTTYHPDPVPGCLDIQOLYWELSQLTH 420
        |||||||
Db      753 PLFOKSSMGPGYLGCOLISLRPEKDGAAATGVDTCTTYHPDPVPGCLDIQOLYWELSQLTH 812
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(11721)
; OTHER INFORMATION: Any "X" = any amino acid
US-10-475-117-162

Query Match 99.1%; Score 2301; DB 6; Length 11721;
Best Local Similarity 99.5%; Pred. No. 1.9e-176;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTSGTPTTVYLGASKTPASIGFSAASHLLILFTLNTITNLRVEENWPG 60
Db 10966 FTHRSSVSTTSGTPTTVYLGASKTPASIGFSAASHLLILFTLNTITNLRVEENWPG 11025
QY 61 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLRPEKDGATGVDICTHRPDPTGP 120
Db 11026 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGSRLLTLLRPEKDGATGVDICTHRPDPTGP 11085
QY 121 GLDREQYLELSQTHSITELGPLYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 11086 GLDREQYLELSQTHSITELGPLYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 11145
QY 181 INNLRYMADMGQPSGLKFNITDNVMKHLSPFLPQRSSLGARYTGCRVIALRSVKNGAETR 240
Db 11146 INNLRYMADMGQPSGLKFNITDNVMKHLSPFLPQRSSLGARYTGCRVIALRSVKNGAETR 11205
QY 241 VDLICTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPYSLDKDSLYLNGYNPEGPDEPPT 300
Db 11206 VDLICTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPYSLDKDSLYLNGYNPEGPDEPPT 11265
QY 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 360
Db 11266 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 11325
QY 361 PLFOKSSMGPFYLGCOLLSLRPEKDGATGVDTTCTHYHPDPVPGGLDIOQLYWELSOLTH 420
Db 11326 PLFOKSSMGPFYLGCOLLSLRPEKDGATGVDTTCTHYHPDPVPGGLDIOQLYWELSOLTH 11385
QY 421 GVTQLGFYVLDROSLFNG 439
Db 11386 GVTQLGFYVLDROSLFNG 11404

RESULT 15
US-10-544-944-1
; Sequence 1, Application US/10544944
; Publication No. US20060134120A1
; GENERAL INFORMATION:
; APPLICANT: Diamandis, Eleftherios P.
; TITLE OF INVENTION: Multiple Marker Assay for Detection of Ovarian Cancer
; FILE REFERENCE: 11757.0088USMO
; CURRENT APPLICATION NUMBER: US/10/544,944
; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: PCT/CA2004/000281
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 60/450,406
; PRIOR FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(11721)
; OTHER INFORMATION: Any "X" = any amino acid
US-10-475-117-162

Query Match 99.1%; Score 2301; DB 6; Length 11721;
Best Local Similarity 99.5%; Pred. No. 1.9e-176;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTSGTPTTVYLGASKTPASIGFSAASHLLILFTLNTITNLRVEENWPG 60
Db 10966 FTHRSSVSTTSGTPTTVYLGASKTPASIGFSAASHLLILFTLNTITNLRVEENWPG 11025
QY 61 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLRPEKDGATGVDICTHRPDPTGP 120
Db 11026 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGSRLLTLLRPEKDGATGVDICTHRPDPTGP 11085
QY 121 GLDREQYLELSQTHSITELGPLYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 11086 GLDREQYLELSQTHSITELGPLYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 11145
QY 181 INNLRYMADMGQPSGLKFNITDNVMKHLSPFLPQRSSLGARYTGCRVIALRSVKNGAETR 240
Db 11146 INNLRYMADMGQPSGLKFNITDNVMKHLSPFLPQRSSLGARYTGCRVIALRSVKNGAETR 11205
QY 241 VDLICTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPYSLDKDSLYLNGYNPEGPDEPPT 300
Db 11206 VDLICTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPYSLDKDSLYLNGYNPEGPDEPPT 11265
QY 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 360
Db 11266 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 11325
QY 361 PLFOKSSMGPFYLGCOLLSLRPEKDGATGVDTTCTHYHPDPVPGGLDIOQLYWELSOLTH 420
Db 11326 PLFOKSSMGPFYLGCOLLSLRPEKDGATGVDTTCTHYHPDPVPGGLDIOQLYWELSOLTH 11385
QY 421 GVTQLGFYVLDROSLFNG 439
Db 11386 GVTQLGFYVLDROSLFNG 11404

RESULT 15
US-10-544-944-1
; Sequence 1, Application US/10544944
; Publication No. US20060134120A1
; GENERAL INFORMATION:
; APPLICANT: Diamandis, Eleftherios P.
; TITLE OF INVENTION: Multiple Marker Assay for Detection of Ovarian Cancer
; FILE REFERENCE: 11757.0088USMO
; CURRENT APPLICATION NUMBER: US/10/544,944
; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: PCT/CA2004/000281
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 60/450,406
; PRIOR FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; TYPE: PRT
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; LENGTH: 22152
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13877)..(13878)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13880)..(13880)
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; LOCATION: (13887)..(13887)
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; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
; LOCATION: (13913)..(13914)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; LOCATION: (14575)..(14575)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; LOCATION: (14579)..(14579)
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; LOCATION: (14581)..(14581)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14587)..(14591)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14593)..(14594)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14725)..(14727)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14731)..(14731)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14735)..(14735)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14737)..(14737)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14743)..(14747)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14749)..(14750)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15661)..(15663)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15667)..(15667)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15671)..(15671)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15673)..(15673)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15679)..(15683)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15685)..(15686)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (15978)..(15978)
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; LOCATION: (15984)..(15984)
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; NAME/KEY: misc_feature
; LOCATION: (15996)..(15997)
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; NAME/KEY: misc_feature
; LOCATION: (16008)..(16008)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; LOCATION: (16017)..(16017)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; LOCATION: (16034)..(16034)
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; OTHER INFORMATION: Xaa can be any naturally occurring amino acid

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; FEATURE:
; NAME/KEY: misc_feature

Query Match 99.1%; Score 2301; DB 6; Length 22152;
Best Local Similarity 99.5%; Pred. No. 4.4e-176;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 21457 SRKNTTTERVLOGLLRPLFKNTSVGLYSGSRUTLLRPEKDGATGVDAICTHRPDPG 21516
Qy 121 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 21517 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 21576
Qy 181 INNLRYMADMGQPGSLKENITDNVKKHLLSPLFQSSLGARYTCRVIALRSVKGAE 240
Db 21577 INNLRYMADMGQPGSLKENITDNVKKHLLSPLFQSSLGARYTCRVIALRSVKGAE 21636
Qy 241 VDLCTYLOPLSGPLPIKQVPHLSQOOTHGITRLGPGYSLDKDSLTVNGYNEPGPDEPPT 300
Db 21637 VDLCTYLOPLSGPLPIKQVPHLSQOOTHGITRLGPGYSLDKDSLTVNGYNEPGPDEPPT 21696
Qy 301 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
Db 21697 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 21756
Qy 361 PLFQKSSMGFFYLGQLISLRPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
Db 21757 PLFQKSSMGFFYLGQLISLRPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 21816
Qy 421 GVTQLGFYVLDRLSLFNG 439
Db 21817 GVTQLGFYVLDRLSLFNG 21835

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Search completed: June 7, 2007, 18:03:08  
Job time : 314 secs

SCORE 2.0 BuildDate: 12/03/2005

SCORE Search Results Details for Application  
10687035 and Search Result  
20070607\_154745\_us-10-687-035-  
1\_copy\_14\_452.rapbm.

Score Home

Retrieve Application

SCORE System

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FAQ

This page gives you Search Results detail for the Application 10687035 and Search Result 20070607\_154745\_us-10-687-035-1\_copy\_14\_452.rapbm.

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OM protein - protein search, using sw model

Run on: June 7, 2007, 17:53:46 ; Search time 188 Seconds  
(without alignments)  
1081.656 Million cell updates/sec

Title: US-10-687-035-1\_COPY\_14\_452

Perfect score: 2321

Sequence: 1 FTHRSSVSTTSTGPTVYL.....HGVTQLGFYLDRLDSLFING 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pcp:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pcp:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pcp:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pcp:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pcp:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2321	100.0	748	5	US-10-687-035-1	Sequence 1, Appli
2	2321	100.0	772	3	US-09-884-441-388	Sequence 388, App
3	2321	100.0	772	3	US-09-907-969-388	Sequence 388, App
4	2321	100.0	772	3	US-09-827-271-388	Sequence 388, App
5	2321	100.0	772	4	US-10-198-053-388	Sequence 388, App
6	2321	100.0	772	5	US-10-860-790-388	Sequence 388, App
7	2321	100.0	809	5	US-10-687-035-2	Sequence 2, Appli
8	2321	100.0	833	3	US-09-884-441-389	Sequence 389, App
9	2321	100.0	833	3	US-09-907-969-389	Sequence 389, App
10	2321	100.0	833	3	US-09-827-271-389	Sequence 389, App
11	2321	100.0	833	4	US-10-198-053-389	Sequence 389, App
12	2321	100.0	833	5	US-10-860-790-389	Sequence 389, App
13	2321	100.0	914	3	US-09-778-320-206	Sequence 206, App
14	2321	100.0	914	3	US-09-910-689-206	Sequence 206, App
15	2321	100.0	914	3	US-09-884-441-312	Sequence 312, App
16	2321	100.0	914	3	US-09-884-441-478	Sequence 478, App
17	2321	100.0	914	3	US-09-907-969-312	Sequence 312, App
18	2321	100.0	914	3	US-09-907-969-478	Sequence 478, App
19	2321	100.0	914	3	US-09-827-271-312	Sequence 312, App
20	2321	100.0	914	4	US-10-010-742-206	Sequence 206, App
21	2321	100.0	914	4	US-10-198-053-312	Sequence 312, App
22	2321	100.0	914	4	US-10-198-053-478	Sequence 478, App
23	2321	100.0	914	4	US-10-714-389-206	Sequence 206, App
24	2321	100.0	914	4	US-10-717-296-206	Sequence 206, App
25	2321	100.0	914	5	US-10-860-790-312	Sequence 312, App
26	2321	100.0	914	5	US-10-860-790-478	Sequence 478, App
27	2317	99.8	1889	4	US-10-142-515-5	Sequence 5, Appli
28	2317	99.8	1890	4	US-10-037-340-217	Sequence 217, App
29	2317	99.8	1890	4	US-10-245-871-314	Sequence 314, App
30	2317	99.8	1890	4	US-10-253-286-314	Sequence 314, App
31	2317	99.8	1890	6	US-11-050-926-217	Sequence 217, App
32	2317	99.8	1890	6	US-11-033-039-314	Sequence 314, App
33	2317	99.8	6995	5	US-10-983-340-4	Sequence 4, Appli
34	2312	99.6	3451	3	US-09-907-969-595	Sequence 595, App
35	2312	99.6	3451	4	US-10-198-053-595	Sequence 595, App
36	2312	99.6	3451	5	US-10-860-790-595	Sequence 595, App
37	2301	99.1	1148	3	US-09-884-441-458	Sequence 458, App
38	2301	99.1	1148	3	US-09-884-441-479	Sequence 479, App
39	2301	99.1	1148	3	US-09-907-969-458	Sequence 458, App
40	2301	99.1	1148	3	US-09-907-969-479	Sequence 479, App
41	2301	99.1	1148	3	US-09-965-738-48	Sequence 48, Appl
42	2301	99.1	1148	3	US-09-827-271-458	Sequence 458, App
43	2301	99.1	1148	4	US-10-097-340-216	Sequence 216, App
44	2301	99.1	1148	4	US-10-198-053-458	Sequence 458, App
45	2301	99.1	1148	4	US-10-198-053-479	Sequence 479, App

ALIGNMENTS

RESULT 1

US-10-687-035-1

; Sequence 1, Application US/10687035

; Publication No. US20050064518A1

; GENERAL INFORMATION:

; APPLICANT: Albione, Earl F.

; APPLICANT: Soltis, Daniel A.

; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED

; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF  
; FILE REFERENCE: 6750-214-999  
; CURRENT APPLICATION NUMBER: US/10/687,035  
; PRIOR FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: 60/485,986  
; PRIOR FILING DATE: 2003-07-10  
; PRIOR APPLICATION NUMBER: 60/418,828  
; PRIOR FILING DATE: 2003-10-12  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 748  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CA 125/0772P 3-repeat  
US-10-687-035-1

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Best Local Similarity 100.0%; Pred. No. 2e-200;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 FTHRSSVSTTPTGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60  
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Qy 61 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120  
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Qy 121 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180  
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Db 134 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193  
  
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Db 374 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQQLYWELSOLTH 433  
  
Qy 421 GVTQLGFYVLDSDSLFING 439  
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Db 434 GVTQLGFYVLDSDSLFING 452

RESULT 2  
US-09-884-441-388  
; Sequence 388, Application US/0988441  
; Patent No. US20020119158A1  
; GENERAL INFORMATION:  
; APPLICANT: Algate, Paul A.

; APPLICANT: Carter, Darrick  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.462C7  
; CURRENT APPLICATION NUMBER: US/09/884,441  
; CURRENT FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 388  
; LENGTH: 772  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-884-441-388

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Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQQLYWELSOLTH 420  
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Db 519 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQQLYWELSOLTH 578  
  
Qy 421 GVTQLGFYVLDSDSLFING 439  
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Db 579 GVTQLGFYVLDSDSLFING 597

RESULT 3  
US-09-907-969-388  
; Sequence 388, Application US/09907969  
; Publication No. US20030091580A1  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steven P.  
; APPLICANT: Retter, Marc W.



; APPLICANT: Fanger, Gary Richard  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Hill, Paul  
; APPLICANT: Albone, Earl  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.462C8  
; CURRENT APPLICATION NUMBER: US/09/907,969  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 596  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 388  
; LENGTH: 772  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-907-969-388

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Best Local Similarity 100.0%; Pred. No. 2.le-200;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 159 FTHRSSVSTTPTGPTTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218  
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QY 61 SRKNTTERTVLOGLLRPLFKNTSGVPLYSGCRLTLRLPEKDGATGDAICTHRPDTGP 120  
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DB 219 SRKNTTERTVLOGLLRPLFKNTSGVPLYSGCRLTLRLPEKDGATGDAICTHRPDTGP 278  
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QY 121 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVSEEPFTLNFT 180  
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DB 279 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVSEEPFTLNFT 338  
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QY 181 INNLRYMADMGQPSGLKFNITDNVKKHLLSPLEFORSSLGARYTGCVRVIALRSVKNGAETR 240  
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DB 339 INNLRYMADMGQPSGLKFNITDNVKKHLLSPLEFORSSLGARYTGCVRVIALRSVKNGAETR 398  
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QY 241 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 300  
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DB 399 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 458  
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QY 301 TPKPATTFLPPLSEATTAKGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360  
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QY 361 PLFKQSSMGPFYLGCOLISLRPEKDGAAATGVTCTTYHPDPVPGGLDIQQLYWELSOLTH 420  
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DB 519 PLFKQSSMGPFYLGCOLISLRPEKDGAAATGVTCTTYHPDPVPGGLDIQQLYWELSOLTH 578  
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DB 579 GVTOLGFYVLDRLDSLFING 597  
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RESULT 4  
US-09-827-271-388  
; Sequence 388, Application US/09827271  
; Publication No. US20030165504A1  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Hill, Paul

; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C6  
; CURRENT APPLICATION NUMBER: US/09/827,271  
; CURRENT FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 388  
; LENGTH: 772  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-827-271-388

Query Match 100.0%; Score 2321; DB 3; Length 772;  
Best Local Similarity 100.0%; Pred. No. 2.le-200;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FTHRSSVSTTPTGPTTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60  
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DB 159 FTHRSSVSTTPTGPTTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218  
|||||  
  
QY 61 SRKNTTERTVLOGLLRPLFKNTSGVPLYSGCRLTLRLPEKDGATGDAICTHRPDTGP 120  
|||||  
DB 219 SRKNTTERTVLOGLLRPLFKNTSGVPLYSGCRLTLRLPEKDGATGDAICTHRPDTGP 278  
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QY 121 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVSEEPFTLNFT 180  
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DB 279 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVSEEPFTLNFT 338  
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DB 339 INNLRYMADMGQPSGLKFNITDNVKKHLLSPLEFORSSLGARYTGCVRVIALRSVKNGAETR 398  
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QY 241 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 300  
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DB 399 VDLICTYLOPLSGPLPIKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 458  
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DB 459 TPKPATTFLPPLSEATTAKGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 518  
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DB 519 PLFKQSSMGPFYLGCOLISLRPEKDGAAATGVTCTTYHPDPVPGGLDIQQLYWELSOLTH 578  
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QY 421 GVTOLGFYVLDRLDSLFING 439  
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DB 579 GVTOLGFYVLDRLDSLFING 597  
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RESULT 5  
US-10-198-053-388  
; Sequence 388, Application US/10198053  
; Publication No. US20030124140A1  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Hill, Paul

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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-388

Query Match      100.0%; Score 2321; DB 4; Length 772;
Best Local Similarity 100.0%; Pred. No. 2.1e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 120
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 278
Qy 121 GLDREQLYLELSQTHSITELGPGYTLDRDSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITELGPGYTLDRDSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 338
Qy 181 INNLRYMADMCGPSLKNITDNVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 240
Db 339 INNLRYMADMCGPSLKNITDNVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 398
Qy 241 VDLCTYQLPSGPGLPKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNFPGDEPPT 300
Db 399 VDLCTYQLPSGPGLPKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNFPGDEPPT 458
Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 518
Qy 361 PLFOKSSGPGFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 420
Db 519 PLFOKSSGPGFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 578
Qy 421 GVTQLGFYVLDRODSLFING 439
Db 579 GVTQLGFYVLDRODSLFING 597

RESULT 6
US-10-860-790-388
; Sequence 388, Application US/106860790
; Publication No. US20050031634A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-860-790-388

Query Match      100.0%; Score 2321; DB 5; Length 772;
Best Local Similarity 100.0%; Pred. No. 2.1e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 120
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 278
Qy 121 GLDREQLYLELSQTHSITELGPGYTLDRDSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITELGPGYTLDRDSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 338
Qy 181 INNLRYMADMCGPSLKNITDNVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 240
Db 339 INNLRYMADMCGPSLKNITDNVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 398
Qy 241 VDLCTYQLPSGPGLPKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNFPGDEPPT 300
Db 399 VDLCTYQLPSGPGLPKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNFPGDEPPT 458
Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 518
Qy 361 PLFOKSSGPGFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 420
Db 519 PLFOKSSGPGFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 578
Qy 421 GVTQLGFYVLDRODSLFING 439
Db 579 GVTQLGFYVLDRODSLFING 597

RESULT 7
US-10-687-035-2
; Sequence 2, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albone, Earl F.
; APPLICANT: Soltis, Daniel A.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
```

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; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860,790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-860-790-388

Query Match      100.0%; Score 2321; DB 5; Length 772;
Best Local Similarity 100.0%; Pred. No. 2.1e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 120
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 278
Qy 121 GLDREQLYLELSQTHSITELGPGYTLDRDSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITELGPGYTLDRDSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 338
Qy 181 INNLRYMADMCGPSLKNITDNVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 240
Db 339 INNLRYMADMCGPSLKNITDNVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 398
Qy 241 VDLCTYQLPSGPGLPKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNFPGDEPPT 300
Db 399 VDLCTYQLPSGPGLPKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNFPGDEPPT 458
Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 518
Qy 361 PLFOKSSGPGFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 420
Db 519 PLFOKSSGPGFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 578
Qy 421 GVTQLGFYVLDRODSLFING 439
Db 579 GVTQLGFYVLDRODSLFING 597

RESULT 7
US-10-687-035-2
; Sequence 2, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albone, Earl F.
; APPLICANT: Soltis, Daniel A.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
```

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; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CA 125/0772P 3-repeat TM
US-10-687-035-2

Query Match      100.0%; Score 2321; DB 5; Length 809;
Best Local Similarity 100.0%; Pred. No. 2.3e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60
    |||||||
Db 14 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 73
    |||||||

Qy 61 SRKENTTERTVQLGLRLPFLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
    |||||||
Db 74 SRKENTTERTVQLGLRLPFLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 133
    |||||||

Qy 121 GLDREQLYLELSQTHSITELGPYTLDRDSLXVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||||||
Db 134 GLDREQLYLELSQTHSITELGPYTLDRDSLXVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
    |||||||

Qy 181 INNLRYADMQPGCSLKFNITDNVNMKLLSPFLQRSSILGARYTGCVRVIALRSVKNGAETR 240
    |||||||
Db 194 INNLRYADMQPGCSLKFNITDNVNMKLLSPFLQRSSILGARYTGCVRVIALRSVKNGAETR 253
    |||||||

Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 300
    |||||||
Db 254 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 313
    |||||||

Qy 301 TPKPATTFLPPLSEATTANGYHLKTLTNFTISNLQYSPDMKGKSGATFNSTEGVLOHLRL 360
    |||||||
Db 314 TPKPATTFLPPLSEATTANGYHLKTLTNFTISNLQYSPDMKGKSGATFNSTEGVLOHLRL 373
    |||||||

Qy 361 PLFKSSMGPFYLCQQLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 420
    |||||||
Db 374 PLFKSSMGPFYLCQQLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 433
    |||||||

Qy 421 GVTQLGFYVLDRLDSLIFNG 439
    |||||||
Db 434 GVTQLGFYVLDRLDSLIFNG 452
    |||||||

RESULT 8
US-09-884-441-389
; Sequence 389, Application US/0988441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
```

```
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-389

Query Match      100.0%; Score 2321; DB 3; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.4e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60
    |||||||
Db 78 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 137
    |||||||

Qy 61 SRKENTTERTVQLGLRLPFLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
    |||||||
Db 138 SRKENTTERTVQLGLRLPFLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 197
    |||||||

Qy 121 GLDREQLYLELSQTHSITELGPYTLDRDSLXVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||||||
Db 198 GLDREQLYLELSQTHSITELGPYTLDRDSLXVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257
    |||||||

Qy 181 INNLRYADMQPGCSLKFNITDNVNMKLLSPFLQRSSILGARYTGCVRVIALRSVKNGAETR 240
    |||||||
Db 258 INNLRYADMQPGCSLKFNITDNVNMKLLSPFLQRSSILGARYTGCVRVIALRSVKNGAETR 317
    |||||||

Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 300
    |||||||
Db 318 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 377
    |||||||

Qy 301 TPKPATTFLPPLSEATTANGYHLKTLTNFTISNLQYSPDMKGKSGATFNSTEGVLOHLRL 360
    |||||||
Db 378 TPKPATTFLPPLSEATTANGYHLKTLTNFTISNLQYSPDMKGKSGATFNSTEGVLOHLRL 437
    |||||||

Qy 361 PLFKSSMGPFYLCQQLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 420
    |||||||
Db 438 PLFKSSMGPFYLCQQLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 497
    |||||||

Qy 421 GVTQLGFYVLDRLDSLIFNG 439
    |||||||
Db 498 GVTQLGFYVLDRLDSLIFNG 516
    |||||||

RESULT 9
US-09-907-969-389
; Sequence 389, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Hill, Paul
```

```
; APPLICANT: Albone, Earl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-969-389

Query Match      100.0%; Score 2321; DB 3; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.4e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTSGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||
Db 78 FTHRSSVSTTSGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137
    |||||||

QY 61 SRKENTTERRVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDTGP 120
    |||||||
Db 138 SRKENTTERRVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDTGP 197
    |||||||

QY 121 GLDREQYLIELSQLTHSITELGPTTLDROSLYVNGFTHRSSVPTTSGVWSEEPFTLNFT 180
    |||||||
Db 198 GLDREQYLIELSQLTHSITELGPTTLDROSLYVNGFTHRSSVPTTSGVWSEEPFTLNFT 257
    |||||||

QY 181 INNLRYMADMGQPGSLKFNITDNVKKHLLSPLEFORSSILGARYTGCRVIALRSVKNGAETR 240
    |||||||
Db 258 INNLRYMADMGQPGSLKFNITDNVKKHLLSPLEFORSSILGARYTGCRVIALRSVKNGAETR 317
    |||||||

QY 241 VDLCTYLOPLSGPLPIKOVFHELSSQOOTHGITRLGPGYSLDKOSLYLNGYNEPGDEPPT 300
    |||||||
Db 318 VDLCTYLOPLSGPLPIKOVFHELSSQOOTHGITRLGPGYSLDKOSLYLNGYNEPGDEPPT 377
    |||||||

QY 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMKGSATFNSTEGVLOHLR 360
    |||||||
Db 378 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMKGSATFNSTEGVLOHLR 437
    |||||||

QY 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 420
    |||||||
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 497
    |||||||

QY 421 GVTOLGFYVLDROSLFING 439
    |||||||
Db 498 GVTOLGFYVLDROSLFING 516

RESULT 10
US-09-827-271-389
; Sequence 389, Application US/09827271
; Publication No. US2003016504A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C8
```

```
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-389

Query Match      100.0%; Score 2321; DB 3; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.4e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTSGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||
Db 78 FTHRSSVSTTSGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137
    |||||||

QY 61 SRKENTTERRVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDTGP 120
    |||||||
Db 138 SRKENTTERRVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDTGP 197
    |||||||

QY 121 GLDREQYLIELSQLTHSITELGPTTLDROSLYVNGFTHRSSVPTTSGVWSEEPFTLNFT 180
    |||||||
Db 198 GLDREQYLIELSQLTHSITELGPTTLDROSLYVNGFTHRSSVPTTSGVWSEEPFTLNFT 257
    |||||||

QY 181 INNLRYMADMGQPGSLKFNITDNVKKHLLSPLEFORSSILGARYTGCRVIALRSVKNGAETR 240
    |||||||
Db 258 INNLRYMADMGQPGSLKFNITDNVKKHLLSPLEFORSSILGARYTGCRVIALRSVKNGAETR 317
    |||||||

QY 241 VDLCTYLOPLSGPLPIKOVFHELSSQOOTHGITRLGPGYSLDKOSLYLNGYNEPGDEPPT 300
    |||||||
Db 318 VDLCTYLOPLSGPLPIKOVFHELSSQOOTHGITRLGPGYSLDKOSLYLNGYNEPGDEPPT 377
    |||||||

QY 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMKGSATFNSTEGVLOHLR 360
    |||||||
Db 378 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMKGSATFNSTEGVLOHLR 437
    |||||||

QY 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 420
    |||||||
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 497
    |||||||

QY 421 GVTOLGFYVLDROSLFING 439
    |||||||
Db 498 GVTOLGFYVLDROSLFING 516

RESULT 11
US-10-198-053-389
; Sequence 389, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
```

```
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-389

Query Match      100.0%; Score 2321; DB 4; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.4e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |
Db 78 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137
    |
Qy 61 SRKFTTERTVLQGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGTP 120
    |
Db 138 SRKFTTERTVLQGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGTP 197
    |
Qy 121 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |
Db 198 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257
    |
Qy 181 INNLRYMADMGQPSGLKFNITDNVWKHLSPPLFORSSLGARYTCRVIALRSVKNGAETR 240
    |
Db 258 INNLRYMADMGQPSGLKFNITDNVWKHLSPPLFORSSLGARYTCRVIALRSVKNGAETR 317
    |
Qy 241 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGITRLGPLYSLDKDSLYLNGYNEPGDPPT 300
    |
Db 318 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGITRLGPLYSLDKDSLYLNGYNEPGDPPT 377
    |
Qy 301 TPKPATTLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
    |
Db 378 TPKPATTLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 437
    |
Qy 361 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
    |
Db 438 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 497
    |
Qy 421 GVTQLGFYVLDROSLFING 439
    |
Db 498 GVTQLGFYVLDROSLFING 516

RESULT 12
US-10-860-790-389
; Sequence 389, Application US/10860790
; Publication No. US20050031634A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860,790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-860-790-389

Query Match      100.0%; Score 2321; DB 5; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.4e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |
Db 78 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137
    |
Qy 61 SRKFTTERTVLQGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGTP 120
    |
Db 138 SRKFTTERTVLQGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPGTP 197
    |
Qy 121 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |
Db 198 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257
    |
Qy 181 INNLRYMADMGQPSGLKFNITDNVWKHLSPPLFORSSLGARYTCRVIALRSVKNGAETR 240
    |
Db 258 INNLRYMADMGQPSGLKFNITDNVWKHLSPPLFORSSLGARYTCRVIALRSVKNGAETR 317
    |
Qy 241 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGITRLGPLYSLDKDSLYLNGYNEPGDPPT 300
    |
Db 318 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGITRLGPLYSLDKDSLYLNGYNEPGDPPT 377
    |
Qy 301 TPKPATTLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
    |
Db 378 TPKPATTLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 437
    |
Qy 361 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
    |
Db 438 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 497
    |
Qy 421 GVTQLGFYVLDROSLFING 439
    |
Db 498 GVTQLGFYVLDROSLFING 516

RESULT 13
US-09-778-320-206
; Sequence 206, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, TongTong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-320-206

Query Match      100.0%; Score 2321; DB 3; Length 914;
Best Local Similarity 100.0%; Pred. No. 2.7e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 159 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218

Qy 61 SRKENTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRDPDTPG 120
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 219 SRKENTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRDPDTPG 278

Qy 121 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 180
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 279 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 338

Qy 181 INILRYMADMGQPGSLKFNITDNVKKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 240
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 339 INILRYMADMGQPGSLKFNITDNVKKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 398

Qy 241 VDLCTYLOPLSGGLPIKQVFHELSSQTHGITRLGPLYSLDKDSLYLINGYNEPGDEPPT 300
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 399 VDLCTYLOPLSGGLPIKQVFHELSSQTHGITRLGPLYSLDKDSLYLINGYNEPGDEPPT 458

Qy 301 TKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMKGKGSATNSTEGVLQHLR 360
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 459 TKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMKGKGSATNSTEGVLQHLR 518

Qy 361 PLFKQSSMGPFYLGQCLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 420
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 519 PLFKQSSMGPFYLGQCLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 578

Qy 421 GVTQLGFYVLDKDSLFING 439
    |||||||||||||||||||
Db 579 GVTQLGFYVLDKDSLFING 597

RESULT 14
US-09-910-689-206
; Sequence 206, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910,689
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; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-689-206

Query Match      100.0%; Score 2321; DB 3; Length 914;
Best Local Similarity 100.0%; Pred. No. 2.7e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 159 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218

Qy 61 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRDPDTPG 120
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 219 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRDPDTPG 278

Qy 121 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 180
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 279 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 338

Qy 181 INILRYMADMGQPGSLKFNITDNVKKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 240
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 339 INILRYMADMGQPGSLKFNITDNVKKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 398

Qy 241 VDLCTYLOPLSGGLPIKQVFHELSSQTHGITRLGPLYSLDKDSLYLINGYNEPGDEPPT 300
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 399 VDLCTYLOPLSGGLPIKQVFHELSSQTHGITRLGPLYSLDKDSLYLINGYNEPGDEPPT 458

Qy 301 TKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMKGKGSATNSTEGVLQHLR 360
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 459 TKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMKGKGSATNSTEGVLQHLR 518

Qy 361 PLFKQSSMGPFYLGQCLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 420
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 519 PLFKQSSMGPFYLGQCLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 578

Qy 421 GVTQLGFYVLDKDSLFING 439
    |||||||||||||||||||
Db 579 GVTQLGFYVLDKDSLFING 597

RESULT 15
US-09-884-441-312
; Sequence 312, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Derrick
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 312

http://es/ScoreAccessWeb/GetItem.action?AppId=10687035&seqId=09323b6780236b2d...
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SCORE Search Results Details for Application 10687035 and Search Result 20070607... Page 17 of 17

; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-884-441-312

Query Match 100.0%; Score 2321; DB 3; Length 914;  
Best Local Similarity 100.0%; Pred. No. 2.7e-200;  
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	FTHRSSVSTSTGCTPTVYLGASKTPASIFGCPASAASHLLILFTLNFTITNLRAYENWMPG	60
Db	159	FTHRSSVSTSTGCTPTVYLGASKTPASIFGCPASAASHLLILFTLNFTITNLRAYENWMPG	218
Qy	61	SRKFNTERVILQGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRDPDTPGP	120
Db	219	SRKFNTERVILQGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRDPDTPGP	278
Qy	121	GLDREQLYLELSQLTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPETLNFT	180
Db	279	GLDREQLYLELSQLTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPETLNFT	338
Qy	181	INNLRVYMDMGQPGSLKFNITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR	240
Db	339	INNLRVYMDMGQPGSLKFNITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR	398
Qy	241	VDLLCTYLQPLSGPLPIKQVFHELSQLQTHGITRLGPISLDKDSLYLNGYNEPGDEPPT	300
Db	399	VDLLCTYLQPLSGPLPIKQVFHELSQLQTHGITRLGPISLDKDSLYLNGYNEPGDEPPT	458
Qy	301	TPKPATTELPPELSEATTAMGYHLKTLTNFTLSNLQYSPDMGKGSATFNSTEGVLQHLR	360
Db	459	TPKPATTELPPELSEATTAMGYHLKTLTNFTLSNLQYSPDMGKGSATFNSTEGVLQHLR	518
Qy	361	PLFKSSKGPFFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQQLYWELSQTH	420
Db	519	PLFKSSKGPFFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQQLYWELSQTH	578
Qy	421	GVTLGFFVLDRLDSLFING	439
Db	579	GVTLGFFVLDRLDSLFING	597

Search completed: June 7, 2007, 18:04:12  
Job time : 190 secs

SCORE 2.0 BuildDate: 12/05/2005

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10687035 and Search Result 20070607

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: June 7, 2007, 17:49:56 ; Search time 41 Seconds  
(without alignments)  
1030.223 Million cell updates/sec

Title: US-10-687-035-1\_COPY\_14\_452  
Perfect score: 2321  
Sequence: 1 FTHRSSVSTTPTGPTVYL.....HGVTQLGFVLDRLSLFING 439

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114.5	4.9	1475	2 S42718	nuclear pore compl
2	105	4.5	630	1 A46149	transcription fact
3	104	4.5	628	1 A39262	transcription fact
4	103.5	4.5	555	2 T00778	probable tRNA aden
5	102.5	4.4	2477	2 S14428	fibronectin precur
6	102	4.4	628	1 A33333	transcription fact
7	101	4.4	1426	2 T30817	homeotic protein C

8	100.5	4.3	1199	2	A40670	nuclear envelope p
9	99.5	4.3	825	2	T29634	hypothetical prote
10	99.5	4.3	1256	1	A43829	muramidase-release
11	99.5	4.3	1443	2	T02491	probable ABC trans
12	99.5	4.3	1777	2	T34369	hypothetical prote
13	99	4.3	650	2	S22835	alpha-agglutinin -
14	99	4.3	693	2	H86214	protein T6D22.6 [1
15	99	4.3	837	2	H72802	minor tail subunit
16	98.5	4.2	967	2	S66852	hypothetical prote
17	98.5	4.2	1020	2	A29355	fibronectin - chic
18	98.5	4.2	1302	2	T23236	hypothetical prote
19	98	4.2	1042	2	S41705	EVI1 protein - hum
20	97	4.2	1051	2	A60191	oncogene Evi-1 - h
21	97	4.2	4936	2	AH2515	hypothetical prote
22	96.5	4.2	2664	2	T28626	variant-specific s
23	96.5	4.2	3078	2	T28432	variant-specific s
24	96	4.1	1260	2	S60896	agglutinin-like pr
25	96	4.1	1747	2	A45974	collagen alpha 1(X
26	96	4.1	1857	2	S31212	collagen alpha 1(X
27	96	4.1	1888	2	S78476	collagen alpha 1(X
28	96	4.1	3570	2	T45025	mucin MUC5B, trach
29	95.5	4.1	559	2	T40764	serine-threonine p
30	95.5	4.1	2121	2	A59233	myosin VII-like pr
31	95.5	4.1	2288	2	T30568	acetyl-CoA carboxy
32	95	4.1	875	2	AF0472	probable outer mem
33	95	4.1	1156	2	T23308	hypothetical prote
34	95	4.1	2508	2	S61441	surface-associated
35	94.5	4.1	995	2	S50358	hypothetical prote
36	94.5	4.1	1355	2	T00075	hypothetical prote
37	94.5	4.1	1787	2	G81684	excinuclease ABC c
38	94.5	4.1	2338	2	I73957	kinase-related pro
39	94	4.0	543	1	ERADGG	fiber protein - ca
40	94	4.0	718	1	ALBSGC	cyclomaltodextrin
41	94	4.0	1408	2	H69068	cell surface glyco
42	94	4.0	2236	1	QZFF	rudimentary protei
43	94	4.0	2386	1	FNHU	fibronectin precur
44	93.5	4.0	537	2	A35400	surface protein T6
45	93.5	4.0	3603	1	D69681	peptide synthetase

ALIGNMENTS

RESULT 1

S42718  
nuclear pore complex protein nup153 - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S42718; S37477  
R:McNorrow, I.; Bastos, R.; Horton, H.; Burke, B.  
Biochim. Biophys. Acta 1217, 219-223, 1994  
A:Title: Sequence analysis of a cDNA encoding a human nuclear pore complex protein, hn  
A:Reference number: S42718; MUID:94154002; PMID:8110839  
A:Accession: S42718  
A:Molecule type: mRNA  
A:Residues: 1-1475 <NCM>  
A:Cross-references: UNIPROT:P49790; UNIPARC:UPI000012FC15; EMBL:Z25535; MID:9406224; P  
Query Match 4.9% Score 114.5; DB 2; Length 1475;  
Best Local Similarity 19.3%; Pred. No. 2.8; Mismatches 149; Indels 133; Gaps 16;  
Matches 80; Conservative 53;



QY	17	TVYLGASKTPTASIFGSPAASHLLILTLNFTITNL	-----YEENWMPGRKFNTE	68
		:   :   :	:   :   :   :   :	
Db	380	SWFKSPLTSG	-----EFRKTORIDNKCSTGYEKNMTPQGNR	419
QY	69	RVYQGLLRPLFKNTSGVPLSGCRLILLRPEKDEATGDAICTHRPDPGGLDRQLY	128	
		:   :   :	:   :   :   :   :	
Db	420	QRESGESYPNES	-----LPAANGLLSSGVGG	454
QY	129	LELSQUTHSIETELGPTYLDROSLYNGCFTHRSSVPT	---TSTGVVSESEPTLNF	183
		:: :   :   :	:   :   :   :   :	
Db	455	AFVASKPIEEEMEVPVPLKSLPITS	-----SSLPTNFSSPEITSPSPINSQALTN	510
QY	184	LRYMADWGQSPKLFENITDYNVKKHLLSPFORSLGARYTCGRVIALRSYKNCATRVDL	243	
		:   :   :   :   :	:   :   :   :   :	
Db	511	KVQMTSPSSTGSPNFKFESSPIKTEANVLPPSSIG	---FTFSVPVAKTAEILOGSST	565
QY	244	LCYTLQPLSGPLPIKQVHELSQOOTHGITRL	-----GPY---SLQKSLY	286
		l:l :   :   :	:   :   :	
Db	566	----LEPI	-----ISSAHHTVTVNSTCKKTPPEDCEGFPFAILKEGV	608
QY	287	LNGYNEPGDEP	-----PTPKPATTELPJLSEATMGYHLKTLTLNFTISNLOY	338
		:   :   :	:   :   :   :   :	
Db	609	LDILKSPGFASPKIDSVAAQPTATSPVWYTRPALS	-----SFSSSGIGFG	653
QY	339	PMCKGSATFNSTGVUQLHLRPLFQKSMGPFYLCQLISLRPEKCATGVDT	393	
		:   :   :	:   :   :   :   :	
Db	654	ESLKAGSSQWCD	-----CLLQNKVTDNKGICACQAAKLSRDPATAKOTGIET	699

```

RESULT 2
A6149
transcription factor HNF-1A - hamster
N:Alternate names: hepatic nuclear factor 1-alpha; transcription factor 1F-B1
C:Species: Cricetinae gen. sp. (hamster)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A46149
R:Emens, L.A.; Landers, D.W.; Moss, L.G.
Proc. Natl. Acad. Sci. U.S.A. 89, 7300-7304, 1992
A:Title: Hepatocyte nuclear factor 1 alpha is expressed in a hamster insulinoma line a
A:Reference number: A46149; MUID:92366449; PMID:1380153
A:Accession: A46149
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-630 <EMC>
A:Cross-references: UNIPROT:Q7MOC7; UNIPARC:UPI0000173313
A:Experimental source: HIT-T15 W.2.2.2 insulinoma cell line
A:Note: sequence extracted from NCBI backbone (NCBIP:110643)
C:Complex: homodimer; can also form heterodimers with, for example, HNF-1B
C:Function:
A:Description: transcription activator required for the expression of a number of liver
A:Note: also expressed in some other tissues, where it may play other roles
C:Superfamily: transcription factor HNF-1; homeobox homology
C:Keywords: DNA binding; homeobox; liver; nucleus; transcription regulation
F:1-33/Region: dimerization
F:222-277/Domain: homeobox homology <HOX>

```

Query Match 4.5%; Score 105; DB 1; Length 630;  
Best Local Similarity 21.4%; Pred. No. 4,2;  
Matches 89; Conservative 55; Mismatches 137; Indels 134; Gaps 20;

Qy	5	SVSVTSTTCTGTTVYLGASKTASIFG-----PSAASHLLI LETLNFPTITNLYE	54
Db	297	ATLSAHSQSPGPTSAIPSKVHGVIYOPATSEAAEVPSSGGPLV-----TVAAPLHQ	350
Qy	55	---ENMWPGSRKFTITGVLLQGLRLPFLKNTSVGLYSGRLTLLRPEKDEATGVDAIC	111
Db	351	VSPGCLPSSSLSTEAKLV-----SATGGPLPPVSTLTAL-----	386
Qy	112	THRPDPTGPGDLREQLYLELSQTHSIT-----ELGP-YTLDRDSLNGE---THRSS	161
Db	387	-HNLEQTSPCLNQOPQNLIWASLPGVMTIGGPEGPASLPFTNTGASTLVIGLASTQAQS	445
Qy	162	VP-----TTSTGVVSEEPPTLNFT-----INLRYMADMGPGSLKFNITD	202
Db	446	VPVINSMGSSLLTLOPVQFSQPLHSPYQOPLPVPVQSHVAQSPFWATMAQ-----	495
Qy	203	NVMKHLISP---LFQRSSIGARTGCRVIALRSVKNGAETRVOLLCTYLOPLSGPLPIKQ	260
Db	496	-----LQSPHALYSHKPEVAQYHTSLPLQTMLI---TDTNLSALSL-----TPTKQ	540
Qy	261	VFHELOOZHGTIRLGPYSYLDKDSLNGYNGPEPDEPTTPKPTATTFPLPLSEATFAMG	320
Db	541	VFTSDTEAS-----SEGPLHESS---PATTIHIHSPQDSSSIQ--	575
Qy	321	YHLK---TTLNFTLN-----IQYSPDWKXG-SATFNSTGVGLQHLRLPFOKS	367
Db	576	-HLOPAHRLSTPTVSSSSIVLYQSSDSTNGSHLLPSNIGHVLETFTQWASS	629

### RESULT 3

A39262  
transcription factor HNF-1A - mouse  
N:Alternate names: hepatic nuclear factor 1-alpha; transcription factor APF; transcrip  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A39262; S70436  
R:Kuo, C.J.; Condev, P. B.; Hsieh, C.L.; Francke, U.; Crabtree, G.R.  
Proc. Natl. Acad. Sci. U.S.A. 87, 9838-9842, 1990  
A:Title: Molecular cloning, functional expression, and chromosomal localization of mou  
A:Reference number: A39262; MUID:91088607; PMID:2263635  
A:Accession: A39262  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-628 <KUO>  
A:Cross-references: UNIPROT:P22361; UNIPARC:UPI0000029283; GB:M57966; NID:g193885; PID  
R:Bach, I.; Pontoglio, M.; Yaniv, M.  
Nucleic Acids Res. 20, 4199-4204, 1992  
A:Title: Structure of the gene encoding hepatocyte nuclear factor 1 (HNF1).  
A:Reference number: S70435; MUID:92375726; PMID:1354855  
A:Accession: S70436  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 199-279 <BAC>  
A:Cross-references: UNIPARC:UPI0000173312  
A:Note: only a part of the nucleic acid sequence is shown  
C:Genetics:  
A:Gene: Hnf-1  
A:Introns: 238/2  
A:Note: the list of introns is incomplete  
C:Complex: homodimer; can also form heterodimers with, for example, HNF-1B  
C:Function: